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OM protein - protein search, using sw model

Run on: October 8, 2003, 17:22:31 ; Search time 55 Seconds
(without alignments)
1477.600 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGSGQAMDGR.....REPARMKGTQADVAEVKQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A.Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2706	100.0	512	21	AA197542 Human obesity prot
2	2580.5	95.4	697	23	AA087087 Sialic acid-bindin
3	2278	84.2	544	23	AA087074 Sialic acid-bindin
4	2265	83.7	544	20	AA141724 Human PRO940 prote
5	2265	83.7	544	21	AA044280 Human PRO940 (UNO4
6	2265	83.7	544	22	AA029082 Human PRO polypept
7	2265	83.7	544	24	AB071170 Human PRO940 prote
8	2265	83.7	544	24	AB065627 Human secreted/tra
9	2265	83.7	544	24	AB065960 Novel human secret

10	2265	83.7	544	24	AB067464 Human secreted/tra
11	2265	83.7	544	24	AB061110 Human PRO940 polyp
12	2265	83.7	544	24	AB065322 Human PRO polypept
13	2265	83.7	544	24	AB058458 Human PRO polypept
14	2265	83.7	544	24	AB055994 Human secreted/tra
15	2265	83.7	544	24	AB056989 Human PRO polypept
16	2265	83.7	544	24	AB010568 Human secreted/tra
17	2220.5	82.1	639	20	AA081023 Human sialoadhesin
18	2220.5	82.1	639	21	AA097543 Human obesity prot
19	2197.5	81.2	639	21	AA025580 CD33-like protein
20	2142.5	79.2	622	23	AA087075 Sialic acid-bindin
21	1960	72.4	475	23	AA014782 Human immunoglobul
22	1929.5	71.3	575	23	AA087072 Sialic acid-bindin
23	1824	67.4	779	23	AA087081 Sialic acid-bindin
24	1824	67.4	779	23	AA087088 Sialic acid-bindin
25	1728	63.9	430	23	AA087077 Sialic acid-bindin
26	1537.5	56.8	312	22	AB016067 Novel human diagn
27	1513.5	55.9	686	23	AB060979 Novel human protel
28	1507.5	55.7	686	24	AA034827 Human Silec-12 pr
29	1451	53.6	619	23	AA087089 Silec-BMS-L3a-hig
30	1443	53.3	667	23	AB060980 Novel human protel
31	1402	51.8	399	20	AA081024 Human sialoadhesin
32	1290	47.7	563	22	AB016065 Novel human diagn
33	1101	40.7	525	22	AB016066 Novel human diagn
34	947	35.0	499	23	AA021547 Silec8-L protein
35	931	34.4	490	23	AB053288 Human polypeptide
36	916	33.9	477	23	AA023674 Silec protein. Und
37	916	33.9	619	23	AB053287 Human polypeptide
38	915	33.8	272	22	AB000220 Novel human diagn
39	909	33.6	595	22	AB070070 Human secreted pro
40	909	33.6	595	23	AB065509 Human albumin fusl
41	900	33.3	466	23	AA087078 Sialic acid-bindin
42	888	32.8	431	20	AA094936 SAF-2 polypeptide
43	888	32.8	431	20	AA094935 SAF-2 polypeptide
44	879	32.5	463	22	AA014529 Human novel protel
45	876	32.4	463	22	AA064077 Human FOAP-9 prote

ALIGNMENTS

```
RESULT 1
ID AA097542 standard; Protein: 512 AA.
XX AA097542:
AC
AC
DT 12-FEB-2001 (first entry)
DT
DT
DE Human obesity protein binding protein-2 homologue #1.
XX
XX
KW Human obesity protein binding protein-2 homologue; HOB-BP2n; obesity;
KW obesity-related disorder; therapy.
XX
XX
OS Homo sapiens.
OS
PN W0200059942-A2.
PN
XX
XX 12-OCT-2000.
PD
PD
PF 22-MAR-2000; 2000MO-US06682.
PF
XX
XX 02-APR-1999; 99US-0127667.
PR
PR
XX
XX (ELIL ) LILLY & CO ELI.
PA
XX Su EW, Wei J;
PI
XX
XX WPI; 2000-664992/64.
DR N-PSDB; AAA37847.
DR
XX
XX New human obesity protein binding protein-2 homologue nucleic acids,
PT polynucleotides and polypeptides useful for producing medicament for
```

PT treating obesity and/or obesity-related disorders
 XX
 PS Claim 9; Page 86-88; 92pp; English.
 XX

CC This sequence is a human obesity protein binding protein-2 homologue
 CC (hob-Bp2h) of the invention. The hob-Bp2h nucleic acids and polypeptides
 CC may be used for the manufacture of a medicament for the treatment of
 CC obesity and/or obesity-related disorders. The hob-Bp2h nucleic acids are
 CC useful as probes or amplification primers in the detection,
 CC quantification or isolation of gene sequences or transcripts, for
 CC recombinant expression of hob-Bp2h polypeptides, as immunogens in the
 CC preparation and screening of antibodies, and in sense or antisense
 CC suppression of one or more hob-Bp2h genes or nucleic acids, host cell
 CC or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and
 CC polypeptides are useful for raising or screening antibodies that
 CC specifically binds to the hob-Bp2h polypeptides.
 CC
 XX Sequence 512 AA;

SO Query Match 100.0%; Score 2706; DB 21; Length 512;
 Best Local Similarity 100.0%; Pred. No. 5.1e-206;
 Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLLSLLSGSQAMGDRFWIRQESVAVPPEGICISVPCSFSTPRDWTGSTPAYGYW 60
 DB 1 MLPLLSLLSGSQAMGDRFWIRQESVAVPPEGICISVPCSFSTPRDWTGSTPAYGYW 60
 QY 61 FKAVETTKGAPVATNHSREVEVSTKRRFQLTGDPKANGSLVIRDAOMODESQYFFRV 120
 DB 61 FKAVETTKGAPVATNHSREVEVSTKRRFQLTGDPKANGSLVIRDAOMODESQYFFRV 120
 QY 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 QY 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 QY 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 241 LVISISRNTDPPRPENLNVMSQANRYLENLNGNTSLPYEGOSLCVCVTHSSPPARL 300
 DB 241 LVISISRNTDPPRPENLNVMSQANRYLENLNGNTSLPYEGOSLCVCVTHSSPPARL 300
 QY 241 LVISISRNTDPPRPENLNVMSQANRYLENLNGNTSLPYEGOSLCVCVTHSSPPARL 300
 DB 241 LVISISRNTDPPRPENLNVMSQANRYLENLNGNTSLPYEGOSLCVCVTHSSPPARL 300
 QY 301 SMTORGQVLSQPDPGVLELPRQVEHEGFTGHAHNPGLSQHVSLSLVHYKKGLIS 360
 DB 301 SMTORGQVLSQPDPGVLELPRQVEHEGFTGHAHNPGLSQHVSLSLVHYKKGLIS 360
 QY 361 TAFSNGAFLGIGITALLFCIALIMKILPKRRTOTETPRPRFSHSTILDYINVPAG 420
 DB 361 TAFSNGAFLGIGITALLFCIALIMKILPKRRTOTETPRPRFSHSTILDYINVPAG 420
 QY 421 PLAQRNOKATPNSRTPPLPGAPSPESKKNOKKOYOLPSPFEPKSTQAPESQSOBEL 480
 DB 421 PLAQRNOKATPNSRTPPLPGAPSPESKKNOKKOYOLPSPFEPKSTQAPESQSOBEL 480
 QY 481 HYATLNPGRVPRPRPARMPKGTQADYAEVKEFQ 512
 DB 481 HYATLNPGRVPRPRPARMPKGTQADYAEVKEFQ 512

RESULT 2
 AAU87087
 ID AAU87087 standard; Protein; 697 AA.

XX AAU87087;
 DT 05-JUN-2002 (first entry)

XX Static acid-binding Ig-related lectin, Siglec-BMS-U3-995-3.

KW Human; static acid-binding Ig-related lectin; SIGLEC; asthma;
 KW Immune system disease; Leukaemia; allergy; Inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;

KW psoriasis; rheumatoid arthritis; conjunctivitis.

XX Homo sapiens.
 OS Synthetic.
 XX

PN W0200208257-A2.

PD 31-JAN-2002.

XX 20-JUL-2001; 2001WO-US23082.

XX 21-JUL-2000; 2000US-220139P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Longphre M, Chang H, Whitney G;

XX WPI: 2002-241565/29.

DR N-PSDB; ABK43373.

PT Novel isolated SIGLEC (static acid-binding Ig-related lectin) protein
 PT molecules useful for treating immune system diseases such as asthma,
 PT leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease

Example 11; Figure 6; 209pp; English.

CC The invention relates to an isolated SIGLEC (static acid-binding Ig-
 CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
 CC are useful for treating immune system diseases such as asthma, leukaemia
 CC or other allergic or inflammatory diseases. Extracellular domains of (I)
 CC represent potential markers for screening, diagnosis, prognosis,
 CC follow-up assays, and imaging methods. (I) is useful as a target for
 CC drugs which inhibit inflammation, tissue damage and remodeling in
 CC asthma, and inflammatory diseases such as allergic rhinitis,
 CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
 CC conjunctivitis, etc. (I) is also useful for monitoring the course of
 CC disease or disorders, and for identifying agents that bind with and/or
 CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
 CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
 CC methods, and to detect the presence and/or amount of SIGLEC-BMS
 CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
 CC (II) are useful as nucleic acid probes are useful for screening genomic
 CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
 CC number is determined for detecting diseases or disorders associated with
 CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
 CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
 CC and in diagnostic imaging technology. AAU87074-AAU87089 represent
 CC human SIGLEC amino acid sequences of the invention.

SO Sequence 697 AA;

Query Match 95.4%; Score 2580.5; DB 23; Length 697;
 Best Local Similarity 73.2%; Pred. No. 6.9e-196;
 Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;

QY 1 MLPLLSLLSGSQAMGDRFWIRQESVAVPPEGICISVPCSFSTPRDWTGSTPAYGYW 60
 DB 1 MLPLLSLLSGSQAMGDRFWIRQESVAVPPEGICISVPCSFSTPRDWTGSTPAYGYW 60
 QY 61 FKAVETTKGAPVATNHSREVEVSTKRRFQLTGDPKANGSLVIRDAOMODESQYFFRV 120
 DB 61 FKAVETTKGAPVATNHSREVEVSTKRRFQLTGDPKANGSLVIRDAOMODESQYFFRV 120
 QY 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 QY 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFELKVTALTKPVDYIPEETLEPGQPVVVICVFNMAFECCPPPSFSW 180
 QY 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPPTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 241 LVISISRNTD----- 252


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Db      241 LVISISRDNTPALEPPQGNVPLYLEAKGQFLRLLCADSQPPATLSWVLQNRVLSSSH 300
      253 -----PENLRVWVSOANRTYLE 270
Db      301 WGRPLGLELPGVKADSGRYTCRAENRLGSGQRAIDLVSQYPPENLRVWVSOANRTYLE 360
      271 NLGNGTSLPYLEGSQSLCVTHSSPPARLSWTORGQVLSPPSDPGVLELPRVOYEHE 330
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      331 GEFTCHARHPLGSOHVSLSLVHY-----354
      421 GEFTCHARHPLGSOHVSLSLVHYSPKRLGPPSCSWAEGHLCSSQASAPSLRWLTGE 480
      355 -----K 355
      481 ELLEGNSQDSFEVTPSSAGPMANSSLSLHGSLGRLRCFAMVNHGAQSGSITLQLPDK 540
      356 KGLISTAFSNGARLIGITALLFLCLALLIMKILPRRTQETPRPRFSHSTILDYIN 415
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      601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKOYOLSPFPEPKSTQAPESOE 660
      476 SOEELHYATLNFPGVRRPREARMKGTQADYAEVKFO 512
      661 SOEELHYATLNFPGVRRPREARMKGTQADYAEVKFO 697

```

RESULT 3

AAU87074 standard: Protein: 544 AA.

AAU87074:

05-JUN-2002 (first entry)

Stallie acid-binding Ig-related lectin, Siglec-BMS-13a.

Human: stallie acid-binding Ig-related lectin; SIGLEC; asthma;

KM tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;

KM psoriasis; rheumatoid arthritis; conjunctivitis.

Homo sapiens.

MO200208257-A2.

31-JAN-2002.

20-JUL-2001: 2001WO-US23082.

21-JUL-2000: 2000US-220139P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Longphre M, Chang H, Whitney G;

WPI: 2002-241565/29.

N-PSDB: ABK43360.

Novel isolated SIGLEC (stallie acid-binding Ig-related lectin) protein

PT molecules useful for treating immune system diseases such as asthma,

PT leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease

CC Claim 5; Figure 2B; 209pp: English.

```

CC are useful for treating immune system diseases such as asthma, leukemia
CC or other allergic or inflammatory diseases. Extracellular domains of (I)
CC represent potential markers for screening, diagnosis, prognosis,
CC follow-up assays, and imaging methods. (I) is useful as a target for
CC drugs which inhibit inflammation, tissue damage and remodeling in
CC asthma, and inflammatory diseases such as allergic rhinitis,
CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
CC conjunctivitis, etc. (I) is also useful for monitoring the course of
CC disease or disorders, and for identifying agents that bind with and/or
CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
CC methods, and to detect the presence and/or amount of SIGLEC-BMS
CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
CC (II) are useful as nucleic acid probes are useful for screening genomic
CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
CC number is determined for detecting diseases or disorders associated with
CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
CC and in diagnostic imaging technology. AAU87074-AAU87089 represent
CC human SIGLEC amino acid sequences of the invention.
XX
XX Sequence 544 AA:
SQ
Query Match 84.2%; Score 2278; DB 23; Length 544;
Best Local Similarity 75.1%; Pred No. 4.9e-172;
Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;
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      1 MLPLLLSLGSGQANDGRFMRVQESVMPGCLISVPCSFSPRODWTGSTPAYGYW 60
      61 FKAVTETTKAPATNHOSEVEMSTRGRQLTGDPKAGCSLYIRDAQODSOFYFRV 120
      61 FKAVTETTKAPATNHOSEVEMSTRGRQLTGDPKAGCSLYIRDAQODSOFYFRV 120
      121 ERGSYRYNFMNDGFLEKVTALTOQPDVYIPETLEPQPVTVICVFEMAREECPSPFSW 180
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      121 ERGSYRYNFMNDGFLEKVTALTOQPDVYIPETLEPQPVTVICVFEMAREECPSPFSW 180
      121 ERGSYRYNFMNDGFLEKVTALTOQPDVYIPETLEPQPVTVICVFEMAREECPSPFSW 180
      181 TGAALSSQGTPTTSHEPSVLSFTPPRODHTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 240
      141 -----VLSFTPPRODHTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 182
      241 LVISISRDNTPD-----252
      183 LVISISRDNTPALEPPQGNVPLYLEAKGQFLRLLCADSQPPATLSWVLQNRVLSSSH 242
      253 -----PENLRVWVSOANRTYLE 270
      243 WGRPLGLELPGVKADSGRYTCRAENRLGSGQRAIDLVSQYPPENLRVWVSOANRTYLE 302
      271 NLGNGTSLPYLEGSQSLCVTHSSPPARLSWTORGQVLSPPSDPGVLELPRVOYEHE 330
      303 NLGNGTSLPYLEGSQSLCVTHSSPPARLSWTORGQVLSPPSDPGVLELPRVOYEHE 362
      331 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAANSNGAFILGITALLFLCLALLIMKILP 390
      363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAANSNGAFILGITALLFLCLALLIMKILP 422
      391 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 450
      423 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 482
      451 NOKKQYOLPSFPPEPKSTQAPESQSEELHYATLNFPGVRRPREARMKGTQADYAEVK 510
      483 NOKKQYOLPSFPPEPKSTQAPESQSEELHYATLNFPGVRRPREARMKGTQADYAEVK 542
      511 FO 512
      543 FO 544

```

RESULT 4

AA41724
 ID AAY41724 standard; Protein; 544 AA.
 XX
 AC AAY41724;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO940 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 .PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99MO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
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 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
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 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
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 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
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 PR 09-APR-1998; 98US-0081195.
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 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083392.
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 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.

PR 29-APR-1998; 98US-0083545.
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 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0083746.
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 PR 07-MAY-1998; 98US-0084600.
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 PR 13-MAY-1998; 98US-0085338.
 PR 15-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 30-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 PI WPI; 1999-551358/46.
 DR N-PSDB; AAZ34109.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 PS
 PS Claim 12; Fig 93; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891 to
 CC AAZ33338, and AAY41685 to AAY41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 CC
 CC
 XX
 XX Sequence 544 AA;

Query Match 83.7%; Score 2265; DB 20; Length 544;
 Best Local Similarity 74.8%; Pred. No. 5, 2e-171;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

OY 1 MLPLILSSILGSSQAMDGRFMRVQESYVMEGLCTISVCSFSYPRQDWTGSTPAYGYW 60
 |||
 Db 1 MLPLILSSILGSSQAMDGRFMRVQESYVMEGLCTISVCSFSYPRQDWTGSTPAYGYW 60
 OY 61 FRAVETTKGAPVATNHOSSREVEMSTRGRFOLTGDPKANGCSLVIRDAQMDESGYFFRV 120

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Db      61 FKAVTETTKGAPVATNHSREVEEMSTGRFQLTGDPKAGKCSLVIIRAQMODESOYFFRV 120
Qy      121 ERGSYVRYNFMNDGFLLKVTALTKQKPDVYIPETLEPGOPVTVCVFMWAECECPSPFSW 180
Db      121 ERGSYVRYNFMNDGFLLKVT----- 140
Qy      181 TGAALSSQGTKPTTSHSVLSFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Db      141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Qy      241 LVISISRDNTPD----- 252
Db      183 LVISISRDNTPALEPOQGNVPYLEAQKGFRLRLCAADSQPATLSWVLQNRVLSSSH 242
Qy      253 -----PENLRVWVSQANRYLE 270
Db      243 WGPRLGLELPVKGADSGRYTCRAENRLGSQORALDLSVOYPPENLRVWVSQANRYLE 302
Qy      271 NLGNSTSLPVLEGOSLCLVCTHSSPPARLSWTORGVLSPOSDPGVLELPRVOYEHE 330
Db      303 NLGNSTSLPVLEGOSLCLVCTHSSPPARLSWTORGVLSPOSDPGVLELPRVOYEHE 362
Qy      331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 390
Db      363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 422
Qy      391 KRRTQETTPRRPRSRHSTIIDYINVTAPLQAKRQKQKTPNSPRPLPPGAPSPSKK 450
Db      423 KRRTQETTPRRPRSRHSTIIDYINVTAPLQAKRQKQKTPNSPRPLPPGAPSPSKK 482
Qy      451 NQKKOYOLPSPFPKSTQAPESQESQELHYATLNPFGVRPPPEARMPKGTQADYAEVK 510
Db      483 NQKKOYOLPSPFPKSTQAPESQESQELHYATLNPFGVRPPPEARMPKGTQADYAEVK 542
Qy      511 FQ 512
Db      543 FQ 544

RESULT 5
AAB44280
ID      AAB44280 standard; Protein: 544 AA.
XX
AC      AAB44280;
XX
DT      08-FEB-2001 (first entry)
XX
DE      Human PRO940 (UNQ477) protein sequence SEQ ID NO:259.
XX
KW      Human: secreted protein; transmembrane protein; PRO; EST: cytosstatic;
KM      expressed sequence tag; detection; cancer.
OS      Homo sapiens.
XX
PN      MO200053756-A2.
XX
PD      14-SEP-2000.
XX
PF      18-FEB-2000; 2000WO-US04341.
XX
PR      08-MAR-1999; 99MO-US05028.
PR      12-MAR-1999; 99US-0123957.
PR      29-MAR-1999; 99US-0126773.
PR      21-APR-1999; 99US-0130232.
PR      28-APR-1999; 99US-0131445.
PR      14-MAY-1999; 99US-0134287.
PR      23-JUN-1999; 99US-0141037.
PR      26-JUL-1999; 99US-0145688.
PR      28-OCT-1999; 99US-0162506.
PR      30-NOV-1999; 99MO-US28313.
PR      02-DEC-1999; 99MO-US28551.
PR      02-DEC-1999; 99MO-US28565.

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PR      16-DEC-1999; 99MO-US30095.
PR      30-DEC-1999; 99MO-US31243.
PR      30-DEC-1999; 99MO-US31274.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00277.
PR      06-JAN-2000; 2000WO-US00376.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI      Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME;
PI      Goddard A, Godowski PJ, Grimaldi CJ, Gunney AL, Hillan KJ;
PI      Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI      Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR      WPI: 2000-611443/58.
DR      N-PSDB: AAC78510.
XX
PT      Novel PRO polypeptides and polynucleotides used in detection methods,
PT      to target bioactive molecules to specific cells, and to modulate
PT      cellular activities -
XX
PS      Claim 12; Fig 93; 636pp; English.
XX
CC      AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC      sequence tag) sequences which encode secreted or transmembrane PRO
CC      polypeptides. The PRO polynucleotides and polypeptides have cytosstatic
CC      activity. The PRO polynucleotides and polypeptides can be used for detecting
CC      the presence of PRO polypeptides in samples, for linking bioactive
CC      molecules to cells and for modulating biological activities of cells,
CC      using the polypeptides for specific targeting. The polypeptide targeting
CC      can be used to kill the target cells, e.g. for the treatment of cancers.
CC      The polypeptide pairs provide specific targeting of bioactive molecules
CC      to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC      the isolation of the PRO polynucleotide sequences.
XX
SQ      Sequence 544 AA;

Query Match      83.7%; Score 2265; DB 21; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy      1 MLPLLLLSLLGSGQADGRFWIRVQSVWMEGLCTVPCSFSPRODMTGSTPAYGYW 60
Db      1 MLPLLLLSLLGSGQADGRFWIRVQSVWMEGLCTVPCSFSPRODMTGSTPAYGYW 60
Qy      61 FKAVTETTKGAPVATNHSREVEEMSTGRFQLTGDPKAGKCSLVIIRAQMODESOYFFRV 120
Db      61 FKAVTETTKGAPVATNHSREVEEMSTGRFQLTGDPKAGKCSLVIIRAQMODESOYFFRV 120
Qy      121 ERGSYVRYNFMNDGFLLKVTALTKQKPDVYIPETLEPGOPVTVCVFMWAECECPSPFSW 180
Db      121 ERGSYVRYNFMNDGFLLKVT----- 140
Qy      181 TGAALSSQGTKPTTSHSVLSFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Db      141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Qy      241 LVISISRDNTPD----- 252
Db      183 LVISISRDNTPALEPOQGNVPYLEAQKGFRLRLCAADSQPATLSWVLQNRVLSSSH 242
Qy      253 -----PENLRVWVSQANRYLE 270
Db      243 WGPRLGLELPVKGADSGRYTCRAENRLGSQORALDLSVOYPPENLRVWVSQANRYLE 302
Qy      271 NLGNSTSLPVLEGOSLCLVCTHSSPPARLSWTORGVLSPOSDPGVLELPRVOYEHE 330
Db      303 NLGNSTSLPVLEGOSLCLVCTHSSPPARLSWTORGVLSPOSDPGVLELPRVOYEHE 362
Qy      331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 390
Db      363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 422

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QY 391 KRRTQTEPRPRESRHSITLIDYINVVPTAGLAKRNRQKATPNSPTLPPLGAPSPESKK 450
Db 423 KRRTQTEPRPRESRHSITLIDYINVVPTAGLAKRNRQKATPNSPTLPPLGAPSPESKK 482
QY 451 NOKKQYOLPSPPEKKSSTQAPESQESQELHYATLNPVGVPRPREARMKGTQADYAEVK 510
Db 483 NOKKQYOLPSPPEKKSSTQAPESQESQELHYATLNPVGVPRPREARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 6
AAU29082
ID AAU29082 standard; Protein: 544 AA.
AC AAU29082;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #59.
XX
XX PRO polypeptide: mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX MO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06520.
XX
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX
XX 03-MAR-2000; 2000US-187202P.
XX
XX 06-MAR-2000; 2000US-186968P.
XX
XX 14-MAR-2000; 2000US-189320P.
XX
XX 14-MAR-2000; 2000US-189328P.
XX
XX 15-MAR-2000; 2000WO-US06884.
XX
XX 21-MAR-2000; 2000US-190828P.
XX
XX 21-MAR-2000; 2000US-191007P.
XX
XX 21-MAR-2000; 2000US-191048P.
XX
XX 28-MAR-2000; 2000US-191314P.
XX
XX 29-MAR-2000; 2000US-192655P.
XX
XX 29-MAR-2000; 2000US-193032P.
XX
XX 30-MAR-2000; 2000US-193053P.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 04-APR-2000; 2000US-194449P.
XX
XX 04-APR-2000; 2000US-194647P.
XX
XX 11-APR-2000; 2000US-195975P.
XX
XX 11-APR-2000; 2000US-196000P.
XX
XX 11-APR-2000; 2000US-196187P.
XX
XX 11-APR-2000; 2000US-196620P.
XX
XX 11-APR-2000; 2000US-196820P.
XX
XX 18-APR-2000; 2000US-198121P.
XX
XX 18-APR-2000; 2000US-198585P.
XX
XX 25-APR-2000; 2000US-199397P.
XX
XX 25-APR-2000; 2000US-199550P.
XX
XX 25-APR-2000; 2000US-199654P.
XX
XX 03-MAY-2000; 2000US-201516P.
XX
XX 17-MAY-2000; 2000WO-US13705.
XX
XX 22-MAY-2000; 2000WO-US14042.
XX
XX 30-MAY-2000; 2000WO-US14941.
XX
XX 02-JUN-2000; 2000WO-US15264.
XX
XX 05-JUN-2000; 2000US-209833P.
XX
XX 28-JUL-2000; 2000WO-US20710.
XX
XX 22-AUG-2000; 2000US-0644848.
XX
XX 24-AUG-2000; 2000WO-US23328.

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PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH ) GENENTECH INC.
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX
XX N-PSDB; AAS45983.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -
XX
XX Claim 11; Fig 118; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
XX detect the presence of a tumour in a mammal by comparing the level of
XX expression of a PRO polypeptide in a test sample of cells from the animal
XX and a control sample of normal cells, whereby a higher level of
XX expression in the test sample indicates the presence of a tumour in the
XX mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
XX and rabbits but are preferably human. The polypeptides can be used to
XX stimulate tumour necrosis factor (TNF) alpha release from human blood,
XX when contacted with it. A specific polypeptide can be used to stimulate
XX the proliferation or differentiation of chondrocyte cells. The PRO
XX proteins can be used to determine the presence of tumours and also
XX CC susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders.
XX
XX Sequence 544 AA:
XX
XX Query Match 83.7%; Score 2265; DB 22; Length 544;
XX Best Local Similarity 74.8%; Pred. No. 5.2e-171;
XX Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
QY 1 MLPLLLSLILGSGQANDGRFWIRQBSVWPEGLICISVCSFSYPRQDMGTSPAYGW 60
Db 1 MLPLLLSLILGSGQANDGRFWIRQBSVWPEGLICISVCSFSYPRQDMGTSPAYGW 60
QY 61 FKAVETTKGAPVATNHOSEVENSTGRQQLTDPKAKGCSLYTRQAQODESQYFRV 120
Db 61 FKAVETTKGAPVATNHOSEVENSTGRQQLTDPKAKGCSLYTRQAQODESQYFRV 120
QY 121 ERGSYVRYNFMNDGFPLKVTALTOKPDVYIPELTLEPQPYVICFENWAFEECPPEFSW 180
Db 121 ERGSYVRYNFMNDGFPLKVT----- 140
QY 181 TGAALSSQGTKPTTSHSVLSFTPRPDHDTDLTCHVDSRRKGVSAQRTVRLVAYAPRD 240
Db 141 -----VLSTPRPDHNTDLTCHVDSRRKGVSAQRTVRLVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALPEPQPGWVPLYLEAKQGFLLKLAADSQPPATLSWLQNRVLSSSH 242
QY 253 -----PPENLRVWVSQANRTVLE 270
Db 243 WGPRLGLELPGVKAGDSGRYTCRAENRRLGSGQRALDLSQYRPENLRVWVSQANRTVLE 302
QY 271 NLGNSTSLPYLEQSLCLVCYVTHSSPPARLSWTQROQVLSPPSQDPGVLELPRVOYEH 330
Db 303 NLGNSTSLPYLEQSLCLVCYVTHSSPPARLSWTQROQVLSPPSQDPGVLELPRVOYEH 362
QY 331 GEFTCHARHPLGSOHSLSLSVYKKGKLISTAFSNGAFIGITALLFLCLALITKTP 390
Db 363 GEFTCHARHPLGSOHSLSLSVYKKGKLISTAFSNGAFIGITALLFLCLALITKTP 422

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OY 391 KRRTQTETPRPRSRHSSTILDYINNVPTAGPLAQKRNOKATPNSPRTPLPPGAPSPESKK 450
    |||||||
Db 423 KRRTQETPRPRSRHSSTILDYINNVPTAGPLAQKRNOKATPNSPRTPPPGAPSPESKK 482
    |||||||
OY 451 NKKKQYQLPSPPEPKSSTQAPESQESQELHATLNPQGVRRPPEARMPKGTQADYAENV 510
    |||||||
Db 483 NKKKQYQLPSPPEPKSSTQAPESQESQELHATLNPQGVRRPPEARMPKGTQADYAENV 542
    |||||||
OY 511 FQ 512
    ||
Db 543 FQ 544

RESULT 7
ABU71170
ID ABU71170 standard; Protein: 544 AA.
AC ABU71170;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO940 protein.
XX
KW Human; PRO; secreted; transmembrane; cytosolic; TNF-alpha; blood;
KM tumour necrosis factor alpha release; chondrocyte cell; proliferation;
XX differentiation; tumour; gene therapy.
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 28-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063420P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 28-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081105P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 28-APR-1998; 98US-083455P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088036P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
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PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 18-JUN-1998; 98US-089653P.
PR 19-JUN-1998; 98US-089908P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 25-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 26-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 01-JUL-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 02-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 04-JUL-1998; 98US-094006P.
PR 04-JUL-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
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Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5,2e-171;
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Db 1 MLPLLLSSLLGSGAMDGKRWIRVOESVMEPEGICISVPSFSYPRDWTGSPRAGYV 60
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61 FKAIVETTKGAPVATINHOSREYEMSTRGRFOLTGDPAGNCSLYTRDAOMODESOYFRRV 120
Db 61 FKAIVETTKGAPVATINHOSREYEMSTRGRFOLTGDPAGNCSLYTRDAOMODESOYFRRV 120
QY 121 ERGSVRYNFMNDGFELVTALTOKPDVYIEETLEPGQPVIVICVFNAFEECEPPPSRW 180
121 ERGSVRYNFMNDGFELVTALTOKPDVYIEETLEPGQPVIVICVFNAFEECEPPPSRW 180
Db 121 ERGSVRYNFMNDGFELVTALTOKPDVYIEETLEPGQPVIVICVFNAFEECEPPPSRW 180
QY 181 TGAALSSOGITKPTTSHEFSVLSFTPRQDHDITLCHVDPSKRGVSAQRTVRLRYAVAPRD 240
181 TGAALSSOGITKPTTSHEFSVLSFTPRQDHDITLCHVDPSKRGVSAQRTVRLRYAVAPRD 240
Db 141 -----VLSFTPRQDHDITLCHVDPSKRGVSAQRTVRLRYAVAPRD 182
141 -----VLSFTPRQDHDITLCHVDPSKRGVSAQRTVRLRYAVAPRD 182
QY 241 LVYISRDNTPD----- 252
241 LVYISRDNTPD----- 252
Db 183 LVYISRDNTPDALBPQGNVPLYDAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSH 242
183 LVYISRDNTPDALBPQGNVPLYDAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PENLRVWVSQANKRVLE 270
253 -----PENLRVWVSQANKRVLE 270
Db 243 WGPRLGLELPGVAKGDSGRYTCRAENRLSGQALDLVQYPPENLRVWVSQANKRVLE 302
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QY 271 NLGNGTSLPYLEGSLCLVCVTHSSPPARLSWTORGVLSPSQSDPGVLELPRVOYEHE 330
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QY 331 GEFTHARHPPLGSGHVSLSIVHKKGLISTAFNSGAFICITALLFLCLALINKILP 390
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QY 451 NOKKOYLPSEPFEPKKSSTOAPESQSEELHYATINPGVRPRPEARMRGSTQADYAEVK 510
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Db 483 NOKKOYLPSEPFEPKKSSTOAPESQSEELHYATINPGVRPRPEARMRGSTQADYAEVK 542
483 NOKKOYLPSEPFEPKKSSTOAPESQSEELHYATINPGVRPRPEARMRGSTQADYAEVK 542
QY 511 FQ 512
511 FQ 512
Db 543 FQ 544
543 FQ 544

RESULT 8

ABU65627 standard; Protein; 544 AA.

AC ABU65627;

DT 19-MAY-2003 (first entry)

DE Human secreted/transmembrane protein, SEQ ID 118.

KW Human; PRO: secreted protein; transmembrane protein;

KW cytosolic; antiarthritic; osteopathic; adrenal tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW cervical tumour; liver tumour; TNF-alpha release; arthritis;

KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;

OS cartilage disorder; sports injury.

XX Homo sapiens.

PN US2003036156-A1.

PR 02-JUL-2002; 2002US-0188767.
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
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PR 01-DEC-1999; 99WO-US28301.
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PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
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PR 18-FEB-2000; 2000WO-US04332.
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PR 01-JUN-2001; 2001WO-US17800.
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PR 09-JUL-2001; 2001WO-US21735.
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PR 10-SEP-1998; 98US-099741P.

Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSSLLGGSCAMGRFWRVQESVNVPEGLICISVPSFSYPRDWTGSPRAYGW 60
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DB 61 FKATETTKGAPVATNHSREVENSTRGRFOLTGPAGNCSLYVRDQOMODESYPFRV 120
QY 121 ERGSVRYNFMNDGFFLKVATLTOKPDVYIPETLEPGQPVYICVFNNAFECPPPSFW 180
DB 121 ERGSVRYNFMNDGFFLKVATLTOKPDVYIPETLEPGQPVYICVFNNAFECPPPSFW 180
QY 121 ERGSVRYNFMNDGFFLKVATLTOKPDVYIPETLEPGQPVYICVFNNAFECPPPSFW 180
DB 121 ERGSVRYNFMNDGFFLKVATLTOKPDVYIPETLEPGQPVYICVFNNAFECPPPSFW 180
QY 181 TGAALSSQGTPTTSHFSVLSTPRPDHDTDLTCHVDTSRKGVSAGQRTVRLRAYABRD 240
DB 141 -----VLSFTPRPDHNTDLTCHVDTSRKGVSAGQRTVRLRAYABRD 182
QY 241 LVYISRDNTD----- 252
DB 183 LVYISRDNTALEPQPOGNVYLEAQGFRLRLCAADSQPPATLSWYLONRYLSSHP 242
QY 253 -----PPENLRVMTSQANRTVLE 270
DB 243 WGPRLGLELPCVKAAGSGRYTCRAENRLGSOQRALDISVYPPENLRVMTSQANRTVLE 302
QY 271 NLNGNTSLPVLGEGSLCYVTHSSPPARLSMTQRGQVLSPOSPDPGVLELPRQVHE 330
DB 303 NLNGNTSLPVLGEGSLCYVTHSSPPARLSMTQRGQVLSPOSPDPGVLELPRQVHE 362
QY 331 GEFTCHAHPLGSOHVSLSLVHYKKGLISTAFSNGAFLGITALLFLCTALLIMKILP 390
DB 363 GEFTCHAHPLGSOHVSLSLVHYKKGLISTAFSNGAFLGITALLFLCTALLIMKILP 422
QY 391 KRRTOTETPRRFSHSTILYINVPYAGPLAQRNOKATPNSRPTLPGAPSPESKK 450
DB 423 KRRTOTETPRRFSHSTILYINVPYAGPLAQRNOKATPNSRPTLPGAPSPESKK 482
QY 451 NOKROYOLPSPPEKSSTOAPESQESQEBELHYATLNFPGVAPRPEARPKSTQADYAEVK 510
DB 483 NOKROYOLPSPPEKSSTOAPESQESQEBELHYATLNFPGVAPRPEARPKSTQADYAEVK 542

QY 511 FQ 512
DB 543 FQ 544

RESULT 9
ABU65960
ID ABU65960 standard; Protein; 544 AA.
AC ABU65960;
XX
XX 20-MAY-2003 (first entry)
DE Novel human secreted and transmembrane protein PR0940.
KW Human; secreted protein; transmembrane protein; cytosolic;
KW gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX Homo sapiens.
OS
XX
XX US2003036157-A1.
PN
XX
PD 20-FEB-2003.
PF
XX
XX 02-JUL-2002; 2002US-0188769.
XX
XX 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 98WO-US05028.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US20111.
PR 15-SEP-1999; 98WO-US21090.
PR 01-DEC-1999; 98WO-US28301.
PR 02-DEC-1999; 98WO-US28551.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUN-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US05020.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
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PR 18-SEP-1997; 97US-059263P.
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PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 04-AUG-1998; 98US-094006P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096871P.
PR 17-AUG-1998; 98US-096891P.
PR 18-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.

Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
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Db      61  FKAATETTKGAPVATINHQSEVEMSTRGFRFULTGDPKAGNSLVIKDAQMODESQYFFRV 120
Oy      121  ERGSVYRRNFMNDGFFLVLTALTKQKPDVYIPEETLEGQPVYIVICVFNNAFECPPPSW 180
Db      121  ERGSVYRRNFMNDGFFLVLT-----140
Oy      181  TGAALSSOGTKPTTSHFSVLSFTPRPDHDTLCTCHVDFSRKVSAGQRTVRLRVAYAPRD 240
Db      141  -----VLSTPRPDHNDTLCTCHVDFSRKVSAGQRTVRLRVAYAPRD 182
Oy      241  LVISISRDNTPD-----252
Db      183  LVISISRDNTPALPEPQGNVPYLEAKQGFLLRLCAADSQPPATLSWLVQNRVLSSSH 242
Oy      253  -----PPENLVVMSQANRYTLE 270
Db      243  WGPRLGLEPGVKAGDSGRYTCRAENRLGSGQALDISVQYPPENLVVMSQANRYTLE 302
Oy      271  NLGNSTSLPYLEGSGSLCVYTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVEHE 330
Db      303  NLGNSTSLPYLEGSGSLCVYTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVEHE 362
Oy      331  GEFTCHAHNPLGSGHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALITKILP 390
Db      363  GEFTCHAHNPLGSGHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALITKILP 422
Oy      391  KRROTETPRPRFSHSTILDIYINVPPTAGPLAQRNKKATPNNSRTLPFGAPSPESKK 450
Db      423  KRROTETPRPRFSHSTILDIYINVPPTAGPLAQRNKKATPNNSRTLPFGAPSPESKK 482
Oy      451  NQKKQYQLSPFPEPKSTQAPESQSELEHATLNFPGVPRPRAPRKGTQADYAEVK 510
Db      483  NQKKQYQLSPFPEPKSTQAPESQSELEHATLNFPGVPRPRAPRKGTQADYAEVK 542
Oy      511  FQ 512
Db      543  FQ 544

RESULT 10
ABU67464
ID      ABU67464 standard; Protein; 544 AA.
XX
AC      ABU67464;
XX
DT      29-MAY-2003 (first entry)
XX
DE      Human secreted/transmembrane protein (PRO) #59.
XX
KW      Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW      tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW      tissue typing.
XX
OS      Homo sapiens.
XX
PN      US2003036162-A1.
XX
PD      20-FEB-2003.
XX
PF      12-JUL-2002; 2002US-0194423.
XX
PR      16-SEP-1998; 98WO-US19330.
PR      07-OCT-1998; 98WO-US21141.
PR      01-DEC-1998; 98WO-US25108.
PR      08-MAR-1999; 99WO-US05028.
PR      14-MAY-1999; 99WO-US10733.
PR      02-JUN-1999; 99WO-US12252.
PR      01-SEP-1999; 99WO-US20111.
PR      15-SEP-1999; 99WO-US21090.
PR      01-DEC-1999; 99WO-US28301.
PR      02-DEC-1999; 99WO-US28551.
PR      30-DEC-1999; 99WO-US31274.
PR      05-JAN-2000; 2000WO-US00219.

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PR      18-FEB-2000; 2000WO-US04341.
PR      18-FEB-2000; 2000WO-US04342.
PR      22-FEB-2000; 2000WO-US04414.
PR      24-FEB-2000; 2000WO-US05004.
PR      01-MAR-2000; 2000WO-US05601.
PR      02-MAR-2000; 2000WO-US05841.
PR      15-MAR-2000; 2000WO-US06884.
PR      30-MAR-2000; 2000WO-US08439.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15264.
PR      28-JUL-2000; 2000WO-US20710.
PR      24-AUG-2000; 2000WO-US23328.
PR      08-NOV-2000; 2000WO-US30952.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000WO-US34956.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
PR      29-AUG-2001; 2001WO-US27099.
PR      26-JUN-1998; 98US-0105413.
PR      07-OCT-1998; 98US-0168978.
PR      06-NOV-1998; 98US-0187368.
PR      07-DEC-1998; 98US-0202054.
PR      03-MAR-1999; 99US-0254311.
PR      14-MAY-1999; 99US-0311832.
PR      25-AUG-1999; 99US-0380137.
PR      25-AUG-1999; 99US-0380138.
PR      25-AUG-1999; 99US-0380139.
PR      25-AUG-1999; 99US-0380142.
PR      18-OCT-1999; 99US-0403297.
PR      12-NOV-1999; 99US-0423844.
PR      22-AUG-2000; 2000US-0644848.
PR      18-SEP-2000; 2000US-0644610.
PR      18-SEP-2000; 2000US-0655350.
PR      08-NOV-2000; 2000US-0709238.
PR      20-DEC-2000; 2000US-0747259.
PR      12-MAR-2001; 2001US-0816744.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      05-JUN-2001; 2001US-0874503.
PR      18-JUL-2001; 2001US-0908827.
PR      30-JUL-2001; 2001US-0918585.
PR      06-AUG-2001; 2001US-0924419.
PR      13-AUG-2001; 2001US-0929404.
PR      16-AUG-2001; 2001US-0931836.
PR      28-AUG-2001; 2001US-0941892.
PR      04-SEP-2001; 2001US-0946374.
PR      15-JAN-2002; 2002US-0052586.

(GETH ) GENENTECH INC.
XX
PA      Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI      Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR      N-PSDB; ACA05758.
XX
WP1: 2003-332039/31.
XX
PT      New secreted and transmembrane PRO polypeptides and nucleic acids,
XX      useful in gene therapy, in chromosome and gene mapping, as chromosome
XX      markers, in tissue typing, and in chromosome identification
XX
PS      Claim 11; Fig 118; 706pp; English.
XX
CC      The invention discloses human nucleic acids encoding secreted and
CC      transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC      specifically binds to the PRO polypeptide, a method for stimulating the
CC      release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC      contacting the blood a PRO polypeptide, a method for stimulating the

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CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in AB067406-AB067710 are the PRO polypeptides of the invention.
XX
SQ Sequence 544 AA;
Query Match 83.78; Score 2265; DB 24; Length 544;
Best Local Similarity 74.86; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
QY 1 MLPLLLSLGSGQAMDRGFWMIRVOESVWVPEGICISVPCSFSPQDMTGSNPAYGYW 60
DB 1 MLPLLLSLGSGQAMDRGFWMIRVOESVWVPEGICISVPCSFSPQDMTGSNPAYGYW 60
QY 61 FKAIVETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSTVIRDAQODESQYFFRV 120
DB 61 FKAIVETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSTVIRDAQODESQYFFRV 120
QY 121 ERGSYVRYNMNMNGEFLKATYALNOKPDVYIPETLEPGQPVYICVFEMAEBCPPPSFSW 180
DB 121 ERGSYVRYNMNMNGEFLKATYALNOKPDVYIPETLEPGQPVYICVFEMAEBCPPPSFSW 180
QY 181 TGAALSSOGTKPTTSHEVSLEFPTPRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 240
DB 181 TGAALSSOGTKPTTSHEVSLEFPTPRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 240
QY 141 -----VSTFPRPODHTDITLCHVDFSRKGVSAORTVRLRYAVAPRD 182
DB 141 -----VSTFPRPODHTDITLCHVDFSRKGVSAORTVRLRYAVAPRD 182
QY 241 LVISISRDNTPD-----PPENIRVWVSQANRYLE 270
DB 241 LVISISRDNTPD-----PPENIRVWVSQANRYLE 270
QY 183 LVISISRDNTPALEPOGNVPLYLEAQKGQFLRLCAADSQPATISWVLQNRVLSSSH 242
DB 183 LVISISRDNTPALEPOGNVPLYLEAQKGQFLRLCAADSQPATISWVLQNRVLSSSH 242
QY 253 -----PPENIRVWVSQANRYLE 270
DB 253 -----PPENIRVWVSQANRYLE 270
QY 243 WGRPRLGLELPYKACDGRYTCRAENRLGSGQRAIDL SVQYPPENIRVWVSQANRYLE 302
DB 243 WGRPRLGLELPYKACDGRYTCRAENRLGSGQRAIDL SVQYPPENIRVWVSQANRYLE 302
QY 271 NLNGSTSLPYLEGOSLCLVCTHSSPPARLSMTORGQVLSPOSDPGVLELPRVOYEHE 330
DB 271 NLNGSTSLPYLEGOSLCLVCTHSSPPARLSMTORGQVLSPOSDPGVLELPRVOYEHE 330
QY 303 NLNGSTSLPYLEGOSLCLVCTHSSPPARLSMTORGQVLSPOSDPGVLELPRVOYEHE 362
DB 303 NLNGSTSLPYLEGOSLCLVCTHSSPPARLSMTORGQVLSPOSDPGVLELPRVOYEHE 362
QY 331 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALELFLCLATIMKILP 390
DB 331 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALELFLCLATIMKILP 390
QY 363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALELFLCLATIMKILP 422
DB 363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALELFLCLATIMKILP 422
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DB 391 KRRTQETTPRRPSRSHSTIIDYINVPYTAFLAQKRNQKATPNSPRTLPFGAPSPSKK 450
QY 423 KRRTQETTPRRPSRSHSTIIDYINVPYTAFLAQKRNQKATPNSPRTLPFGAPSPSKK 482
DB 423 KRRTQETTPRRPSRSHSTIIDYINVPYTAFLAQKRNQKATPNSPRTLPFGAPSPSKK 482
QY 451 NOKKOYOLPSPPEKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 510
DB 451 NOKKOYOLPSPPEKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 510
QY 483 NOKKOYOLPSPPEKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 542
DB 483 NOKKOYOLPSPPEKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544
RESULT 11
AB061110
ID AB061110 standard; Protein: 544 AA.
XX
AC AB061110;
XX
DT 08-MAY-2003 (first entry)

XX
DE Human PRO940 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW Immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antitumour;
KW antithrombotic; anti-tumour; antineoplastic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
XX
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US050190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US15264.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06550.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077633P.
PR 11-MAR-1998; 98US-077641P.
PR 12-MAR-1998; 98US-077649P.
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PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.

PR 27-MAR-1998; 98US-079663P.
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 PR 27-MAR-1998; 98US-079786P.
 PR 30-MAR-1998; 98US-079920P.
 PR 30-MAR-1998; 98US-079923P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-0040220.
 PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.
 PR 10-MAR-1999; 99US-0265686.
 PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380142.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.
 XX
 XX (GENENTECH INC.
 XX
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ;
 PI Klayavin U, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PW, Wood WT;
 XX WPI: 2003-288163/28.
 DR N-PSDB; ABX92481.
 PR Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies
 XX
 XX Claim 12; Fig 93; 459pp; English.
 CC
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC ABU61071-ABU61164 represent the human PRO polypeptides of the
 CC invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at

CC segdata.uspto.gov/psipsdIdentEntry.html.
 XX
 SQ Sequence 544 AA:
 Query Match 83.7%; Score 2265; DB 24; Length 544;
 Best Local Similarity 74.8%; Pred. No. 5, 2e-171;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
 QY 1 MLPLILSSLLGSGAMQGRFWIRQVQESYVMEVGLICISVPCFSFIPRODWTGTPATGW 60
 DB 1 MLPLILSSLLGSGAMQGRFWIRQVQESYVMEVGLICISVPCFSFIPRODWTGTPATGW 60
 QY 61 FKAVETTKGAPVATNHSREVEVMSRGRFOLGTPAGNCSLVTRDQOMQDESQYFV 120
 DB 61 FKAVETTKGAPVATNHSREVEVMSRGRFOLGTPAGNCSLVTRDQOMQDESQYFV 120
 QY 121 ERGSYVRYNFMNDGFELKVTALTKRPDYIIPETLEPGQPVYIVCFMNAFEECPPEPSFW 180
 DB 121 ERGSYVRYNFMNDGFELKVTALTKRPDYIIPETLEPGQPVYIVCFMNAFEECPPEPSFW 180
 QY 181 TGAALSSQGTKEPTTSHFVSLFPPRPOHDDDLTCHVDFSKRGVAQRTVLRVAYAPRD 240
 DB 181 TGAALSSQGTKEPTTSHFVSLFPPRPOHDDDLTCHVDFSKRGVAQRTVLRVAYAPRD 240
 QY 141 -----VLSFTPRPODHNTDLTCHVDFSKRGVAQRTVLRVAYAPRD 182
 DB 141 -----VLSFTPRPODHNTDLTCHVDFSKRGVAQRTVLRVAYAPRD 182
 QY 241 LVISIRNDTPD----- 252
 DB 241 LVISIRNDTPD----- 252
 QY 183 LVISIRNDTPALEPQPGQNVYLEAQKQFLRLCAADSQPPLLSVNLQNVLSSSH 242
 DB 183 LVISIRNDTPALEPQPGQNVYLEAQKQFLRLCAADSQPPLLSVNLQNVLSSSH 242
 QY 253 -----PENLRVMSQANRTVLE 270
 DB 253 -----PENLRVMSQANRTVLE 270
 QY 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSQLALDLSVQYPPENLRVMSQANRTVLE 302
 DB 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSQLALDLSVQYPPENLRVMSQANRTVLE 302
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 DB 271 NLNGSTSLPVLEGOSLCVCTHSSPPARLSMTQGVLSQSPDPGVLELPRVQVHE 330
 QY 303 NLNGSTSLPVLEGOSLCVCTHSSPPARLSMTQGVLSQSPDPGVLELPRVQVHE 362
 DB 303 NLNGSTSLPVLEGOSLCVCTHSSPPARLSMTQGVLSQSPDPGVLELPRVQVHE 362
 QY 331 GEFTCHAHHPGLSGQVHSLSLSVHYKKGLISTAFSGAFLGIGITLALFLCALILMKILP 390
 DB 331 GEFTCHAHHPGLSGQVHSLSLSVHYKKGLISTAFSGAFLGIGITLALFLCALILMKILP 390
 QY 363 GEFTCHAHHPGLSGQVHSLSLSVHYKKGLISTAFSGAFLGIGITLALFLCALILMKILP 422
 DB 363 GEFTCHAHHPGLSGQVHSLSLSVHYKKGLISTAFSGAFLGIGITLALFLCALILMKILP 422
 QY 391 KRRITETPPRPFSSHSTILDTINVPYAPGLAQKRNKATPNSRFTPLPGADSPESKK 450
 DB 391 KRRITETPPRPFSSHSTILDTINVPYAPGLAQKRNKATPNSRFTPLPGADSPESKK 450
 QY 423 KRRITETPPRPFSSHSTILDTINVPYAPGLAQKRNKATPNSRFTPLPGADSPESKK 482
 DB 423 KRRITETPPRPFSSHSTILDTINVPYAPGLAQKRNKATPNSRFTPLPGADSPESKK 482
 QY 451 NOKKOYOLPSPPEPSSIQAPESQSOEELHYATLNPFGVPRPRAPRMKGMQADYAEVK 510
 DB 451 NOKKOYOLPSPPEPSSIQAPESQSOEELHYATLNPFGVPRPRAPRMKGMQADYAEVK 510
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 XX 16-MAY-2003 (first entry)
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 KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
 KW chondrocyte differentiation; chondrocyte proliferation; tumour.
 XX Homo sapiens.
 OS
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 XX 13-FEB-2003.
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PF 17-JUN-2002; 200205-0173697.
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Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5,2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
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DB 61 FKAVTETTKGAPVATNHOSEVENSTRGRFOLTGDPKAGNCSLYIRDAKOMODESQYFRV 120
QY 121 ERGSYVRNFMNDGFFLKVTALTKRPDYIPEETLEPGQPTVICVFNMWAFEECPPEPSFSW 180
DB 121 ERGSYVRNFMNDGFFLKVTALTKRPDYIPEETLEPGQPTVICVFNMWAFEECPPEPSFSW 180
QY 181 TGAALSSQGTPTTSHFSVLSFTPRPODHTDLCHVDESRKGYSAQRTVRLRAYAPRD 240
DB 141 -----VLSFTPRPODHTDLCHVDESRKGYSAQRTVRLRAYAPRD 182
QY 241 LVISISRDNTPD----- 252
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QY 253 -----PENIRVMVSQANRTVLE 270
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QY 271 NLNGTSLPYLEGOSLVCVTHSSPPARLSWTRQGVLSPSQSDGCVLELPRVQVEHE 330
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QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGIGTALLFLCLALIMKILP 390
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QY 511 FQ 512
DB 543 FQ 544

RESULT 13
ABU58458 standard; Protein: 544 AA.
ABU58458;
AC ABU58458;
DT 15-APR-2003 (first entry)
DE Human PRO polypeptide #59.
KW Human; PRO: cytosolic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADPRT;
KW antibody-dependent enzyme mediated prodng therapy.
OS Homo sapiens.
PN US2003027272-A1.
PD 06-FEB-2003.
PE 21-JUN-2002; 2002US-0176492.
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QY 511 FQ 512
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Db 543 FQ 544

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RESULT 14

ABU55994 ID ABU55994 standard; Protein; 544 AA.

AC ABU55994;

DT 26-MAR-2003 (first entry)

DE Human secreted/transmembrane protein, PRO940.

XX Human; secreted protein; transmembrane protein; PRO;

KW antiarthritic; vulnary; tumour necrosis factor- α ;

KW chondrocyte cell proliferation; chondrocyte cell differentiation;

KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;

KW prostate tumour; rectal tumour; cervical tumour; liver tumour;

XX bone disorder; cartilage disorder; arthritis; sports injury.

XX Homo sapiens.

XX OS US2003022298-A1.

XX PD 30-JAN-2003.

XX PF 20-JUN-2002; 2002US-0176913.

XX PR 05-NOV-1997; 97WO-US20069.

PR 10-SEP-1998; 98WO-US18824.

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PR 14-SEP-1998; 98WO-US19177.
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Query Match 83.7%: Score 2265; DB 24; Length 544;

Best Local Similarity 74.8%: Pred. No. 5.2e-171; Indels 148; Gaps 2;

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DB 61 FKAVETTKAPATVATNQSREVENSTGRFQLTGDPKAKKCSLYIRAQMODSQTFRV 120
QY 121 ERGSYVYNNMNGGFLKVTALQKPDVYIPELTLPQPVYICVFNMAFECCPPSFSW 180
DB 121 ERGSYVYNNMNGGFLKVT----- 140
QY 121 ERGSYVYNNMNGGFLKVTALQKPDVYIPELTLPQPVYICVFNMAFECCPPSFSW 180
DB 121 ERGSYVYNNMNGGFLKVT----- 140
QY 181 TGAALSSQGTAKPTTSHEVSLSFTPRPODHDITLCHVDFSRKGVSAQRTVRLRYAVAPRD 240
DB 141 -----VLSFTPRPODHDITLCHVDFSRKGVSAQRTVRLRYAVAPRD 182
QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPDLEPOQGNVPLYEAKGQFLRLCAADSOPTATLSWLONRVLSSSH 242
QY 253 -----PPENLRVWVSQANRTVLE 270
DB 243 WGPRLPLGLHDPYKAGDSGRYTCRAENRRLSQQRALDLSVQYPPENLRVWVSQANRTVLE 302
QY 271 NLGNGTSLPVLEGOSLVCVTHSSPPARLSWTORGVLSPSOPSDGVLELRPVQVHE 330
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QY 331 GEFTCHARHPLGSHVLSLSVHKKKLLISTAFSNGAFLLIGTALLFLCLALIMILP 390
DB 363 GEFTCHARHPLGSHVLSLSVHKKKLLISTAFSNGAFLLIGTALLFLCLALIMILP 422
QY 391 KRRTOTETPPRPSRHSSTIIDYINVTAGPLAQKRAQKATPNSPRTPLPGAPSPSSKK 450
DB 423 KRRTOTETPPRPSRHSSTIIDYINVTAGPLAQKRAQKATPNSPRTPLPGAPSPSSKK 482
QY 451 NOKKOYOLPSFPEPKSSTQAPESQESQEEHLVATLNFPGVPRPEARMKGTQADVAEVK 510
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QY 511 FQ 512
II
Db 543 FQ 544

RESULT 15
ABU56989
ID ABU56989 standard; Protein; 544 AA.
XX
XX ABU56989;
AC
XX 04-APR-2003 (first entry)
DT
XX
XX Human PRO polypeptide #59.
DE
XX
XX Human; PRO; tumour necrosis factor-alpha; blood; cancer;
KW chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;
KW kidney; rectum; cervix; liver; bone disorder; cartilage disorder;
KW arthritis; sports injury; genetic disorder; antiarthritis; vulnerary.
OS Homo sapiens.
XX
XX US2003027280-A1.
PN
XX 06-FEB-2003.
PD
XX
XX 20-JUN-2002; 2002US-0176993.
PF
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DB 141 -----VLSFPPRODHTDLCVHDFSSKGSQAQTVLRVAYAPRD 182
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DB 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSOGRALDLSYQPPENLRVMSQANRTVLE 302
QY 271 NLGNGTSLPYLEGSLCLVCVTHSSPPARLSMTORGVLSPSQSDPGVLELPRVOYEHE 330
DB 303 NLGNGTSLPYLEGSLCLVCVTHSSPPARLSMTORGVLSPSQSDPGVLELPRVOYEHE 362
QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIMKILP 390
DB 363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIMKILP 422
QY 391 KRRTOTETPPRPSRHSHTIIDYINVPYAGPLAOKRNQKATPNSPRTPLPPGAPSPESKK 450
DB 423 KRRTOTETPPRPSRHSHTIIDYINVPYAGPLAOKRNQKATPNSPRTPLPPGAPSPESKK 482
QY 451 NOKKQYOLPSPPEKKSSTOAPESQSEELHYATLNPVGRPREARMKGTQADYAEVK 510
DB 483 NOKKQYOLPSPPEKKSSTOAPESQSEELHYATLNPVGRPREARMKGTQADYAEVK 542
QY 511 FO 512
DB 543 FO 544

```

Search completed: October 8, 2003, 20:01:58
 Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 19:49:12 : Search time 30 Seconds
(without alignments)
1641.279 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLLSLILGSGQAMDGR.....REPARMPKQTQADVAEVKRFQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	694	25.6	364	A30521	myeloid cell surfa
2	528	19.5	403	I52590	m3-B isoform - mo
3	304.5	11.3	626	A61084	myelin-associated
4	302.5	11.2	620	JH0593	Schwann cell myel
5	295.5	10.9	626	BNRT3	myelin-associated
6	289.5	10.7	582	BNRT3S	myelin-associated
7	288.5	10.7	637	B33785	myelin-associated
8	245	9.1	1594	S50065	sialoadhesin - mou
9	227	8.4	862	I49583	differentiation an
10	220.5	8.1	868	A46512	CD22 homolog/B lym
11	206.5	7.6	647	A35648	B-cell adhesion pr
12	202.5	7.5	847	JH0371	B-cell adhesion pr
13	186	6.9	526	A32164	biliary glycoprote
14	184	6.8	402	T05062	probable advanced
15	180	6.7	4391	A38096	perlecan precursor
16	167	6.2	321	JH0395	biliary glycoprote
17	167	6.2	351	JH0396	biliary glycoprote
18	167	6.2	417	JH0394	biliary glycoprote
19	167	6.2	464	C30127	transmembrane carc
20	156.5	5.8	336	C27658	pregnancy-specific
21	153	5.7	3707	S16252	heparan sulfate pr
22	153.5	5.7	416	A42879	advanced glycosyla
23	151.5	5.6	1241	T37190	nephrit - human
24	149	5.5	210	JC4122	pregnancy-specific
25	149	5.5	538	JC3457	vascular cell adhe
26	148.5	5.5	5175	T20992	hypochetlcal prote
27	148.5	5.5	5198	T43290	hemiscntin precurs
28	147.5	5.5	1906	S68235	myosin-light-chain
29	147	5.4	332	JN0067	pregnancy-specific

30	144.5	5.3	26926	1	I38344
31	143	5.3	702	2	A36319
32	142.5	5.3	1232	2	T43027
33	141.5	5.2	739	2	JN0581
34	141	5.2	402	2	A54312
35	140.5	5.2	392	1	RMHUPD
36	140.5	5.2	417	1	RMHUPA
37	140.5	5.2	428	2	J50032
38	140.5	5.2	428	2	I57486
39	140	5.2	521	2	S34338
40	140	5.2	628	2	I38000
41	139.5	5.2	419	2	JC4123
42	139	5.1	404	1	I61596
43	138.5	5.1	349	2	A34815
44	138.5	5.1	495	2	A55181
45	138	5.1	324	2	G43354

ALIGNMENTS

RESULT 1

A30521
Myeloid cell surface antigen CD33 precursor - human
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 29-Aug-1997
C:Accession: A30521
R:Simmons, D.; Seed, B.
J. Immunol. 141, 2797-2800, 1988
A:Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid prog
A:Reference number: A30521, MUID:89009814; PMID:3139766
A:Accession: A30521

A:Molecule type: mRNA
A:Residues: 1-364 <SI>
C:Genetics:
A:Gene: GDB:CD33
A:Cross-references: GDB:119762; OMIM:159590
A:Map position: 19q13.3-19q13.4
C:Superfamily: Immunoglobulin homology
C:Keywords: glycoprotein; surface antigen; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-259/Domain: extracellular #status predicted <Ext>
F:260-282/Domain: transmembrane #status predicted <TM>
F:283-364/Domain: intracellular #status predicted <CYT>
F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	Score	DB 2	Length	364
Best local Similarity	32.8%	Pred. No. 4.3e-40		
Matches	168	Conservative	59	Mismatches 137; Indels 148; Gaps 8;
OY	1	MLPLLLSLILGSGQAMDGRFWIRVOESVNVPEGLCTISVPCSFSTPRDMTGSTPAYGW	60	
DB	1	MLPLLLPLMLGALMDPRFWLQVOESVYVGGILVLCFFHPIPYDKNSPVHGW	60	
OY	61	FKAVETTKGAPATNHQSEVEMSTRGRFOLGDPKAGKCSVIRDAOMDQSEFFRV	120	
DB	61	FREGAIIISGDSFPAITKKLDOEVOETQGRRLGDSRNKCSISTVDARRDQSTFFRM	120	
OY	121	ERGSYVRNFMNDGFILKYALTOKRPDVYIPETLEBQOPVTVCFVNMAFEECPSPFSM	180	
DB	121	ERGS-FTKYSKSPQLSVHTVTLTHNRKILIPGLERGHKNLCSVSMACEGTPPIFSM	179	
OY	181	TGAAISSQGTKPTTSFVSFTFPRQDHDITLCHVDSRKGVSAQRVRLAVAPRD	240	
DB	180	LSAAPSTLG--PRTTSSVLLITPRQDHTNLTCCVFRAGAVTTERITQLNVTVPON	237	
OY	241	LVTISRDNTPPPENLRVWVSQANRTVLLENIGTSLPLLEGQSLCLVCVTHSSPARL	300	
DB	238	PITGTRP-----GDC-----	247	
OY	301	SWTORGQVLSPPSPDQVLELPRVQVEHEGEFTCHARPLASQHVLSLVHYKKGLIS	360	
DB	248	-----SGKQETRAVV-----	258	


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Oy      462 PEPKSTQAPESQSEQELHYATLNFPGVRPPPEARMPKGTQADYAEVK 510
          : : | | : : | | : : | | | | :
Db      587 -----RGEPELDTSYSHSDL-GKRPTKDSYTLSEELAEYAEIR 624

```

RESULT 4

Schwann cell myelin protein precursor - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: JH0593; PS0356
R:Initial: C.; Tropek, M.B.; Cameron-Curry, P.; Rossler, J.; Marshak, D.R.; Roder, J.; Le
Neuron 8, 323-334, 1992
A:Title: Molecular characterization of the schwann cell myelin protein, SMP: structural
A:Reference number: JH0593; MUID:92153423; PMID:1739462
A:Accession: JH0593

A:Cross-references: GB:S8311, NID:g245729, PIDN:AB21466.1, PID:g245730
A:Experimental source: spinal cord
A:Note: the species of quail is not identified
A:Accession: PS0356
A:Molecule type: protein

A:Residues: 18-31;119-132;135-157;563-566,'x','x'><DUI>
C:Comment: This protein is expressed on all external membranes of Schwann cells
C:Superfamily: myelin-associated glycoprotein; Immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
E:1-17/Domain: signal sequence <status predicted >Sig>
E:18-650/Product: Schwann cell myelin protein <status predicted >Sig>
F:33-101/Domain: Immunoglobulin homology <TM>
F:505-533/Domain: transmembrane <status predicted >TM>
F:222,314,'331',405,'443'/Blinding site: carboxylate (Asn) (covalent) #status predicted

Query Match

Query Match	11.2%	Score 302.5	DB 2	Length 620
Best Local Similarity	22.4%	Pred. No. 4.7e-13		
Matches 148; Conservative	89;	Mismatches 224;	Indels 199;	Gaps 29

QY LLLSLTLGGSSQAMDGDEFFNTRVQESVMEPEGICISVPCFSFSPRODMTGSPRAY--GWFK 62
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
D 4 LVLTVLMTGTCISAPMAAMPKMAALSGTCVQLPCRFDPEE-----LRASLIGGLMY- 58

OY ATLETTKGP-----VATTHQSREVMSTRGRFLQTGDPAAGCSLYTRQMD- 113
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 59 -----EGSPYRKNTPRVVANRSBSAVHSEFAGAASTLGDPGTGRDLTNT--ARLSLE 110

OY 114 -SQYFFRVERGSYYVRNFMNDGFFLKVLTALQKPDVYIPETLEPGQPVTVICVFNNMAFEE 172Z
 : : : : : : : : : : : : : : : : : : :
DB 111 AGKYFRGRGLGGVGNYSF-SHAEILDVMA---APHLVEPHLEVAGSEAEITCRVP---DN 1633

OY 173 CPP--PSFSWTGA--ALSSGQTK-----DPTSHSVLSFMPRPDDHTDLTCWVDSRK 222
||| : ||| | : | : ||| : | : | :
Db 164 CPLLRLPLTWGTTEELLDPICKERIEDLGSKSLGLSRPPRKEIDGRVACGWPFINS 223

[illegible]

```

OY      254 PENURVMYSQAN-----RTVLEN-----LONGTSLPYLEGOSTL 2866
          |||:::|           | ||
284  GPNT I I I SNGDDGCSFECVAEUDUCBUBRSTOI BUAVABPAVRUG -CTIHCENDDU 3423
          :|||:::|           : |||:::|

```

287 CLVCVTHSSPPARLSWTOKGOVLSQSPSPGVLELPVROYEHGEFTCHARHPLGSOHV 346

```

D6      343 SVYCKRAESEPAALIVLRGKQVMAAIEDYHTMEMRPARPEDGCTYSCVAENQHGASST 402
OY      347 SLSTSVHYKKGLI-----STAF----- 363
        |::|| |:: | |

```

Db 403 SFNISEVEYPPVLPRASRCTAGGDDVRCVCWNSIPDSSSLVELELTRQTVDGHRDETA 4622

QY 364 ---SNGAFLGIGIT-----ALLFLCLALIMKILPKRRTQETEPAPRFRRH----- 4066

Db 463 PPGSDGSIIGI-LTLRGPLEPRLVCA-----RNRGTTAROLRFHHPGGLVYAK 513

```

QY 407 ---STLLIYINVPAGLACKRNNKATPPNSPRPLPP-----GAPSPESKKNQ-----452
      ::: ::: ::: ::: ::: :::
Db 514 VGPVGAVVAFAIYIAIVCYLSSQRRKKKAGSEVTPYVPMAGPCGDDPLDLRQCVWMLR 573
      ::: ::: ::: ::: ::: :::
QY 453 --KKQQLPSPFPEPKSSTOAPESQSOEELHATLTFNGVGPVPREARPMKQTQADYAEVK 510
      ::: ::: ::: ::: ::: :::
Db 574 GAMERKAL---GVVEGSGAP--QETVTPSH-----PYMK--TKGLPEDDPEVAEIR 618
      ::: ::: ::: ::: ::: :::

```

RESULT 5

myelin-associated glycoprotein precursor long splice form - rat
N.Alternate names: 1k236; brain neuron cytoplasmic protein 3; MAG
C.Species: Rattus norvegicus (Norway rat)
C.Date: 19-Feb-1994 #sequence revision 31-Dec-1989 #text change 01-Dec-2000
C.Accession: A29028; A94175; A27185; A90886; I55564; I52892; A03138; A26362
R.Lab: C. Brown, M.A. Nave, K.A. Norstrom, A.B. Quarles, R.H. Bloom, F.E. Milner
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A.Title: Two forms of 1k236/myelin-associated glycoprotein, a cell adhesion molecule
I.Reference numbers: A29028; MUID:87232001; PMID:2436699

A:Accession: A29028
A:Molecule_type: mRNA
A:Residues: 1-626 <LB>
A:Cross-references: GB:M16600; NID:g205269; PIDN:AAA1557.1; PID:g205270
R:Aquint, M.; Koder, J.; Chia, L.-S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, F.
P:Proc. Natl. Acad. Sci. U.S.A. 84, 600-604, 1987
A:Title: Molecular cloning and primary structure of myelin-associated glycoprotein
R:Reference number: A94175; MUID:87092455; PMID:2432614

A:Accession: AY4175
A:Molecule type: mRNA
A:Residues: 1-626 <ARO>
A:Cross-references: GB:MI4871; NID:q205267; PIDD:AA1556.1; PID:q205268
R:Salzer, J.L.; Holmes, M.P.; Colman, D.R.
J. Mol. Biol. 1992

U. Cell Biol. 104, 357-363, 1997

A. Title: The amino acid sequences of the myelin-associated glycoproteins: homology to

A. Reference number: A27185; MUID: 87166195; PMID: 2435742

A:Accession: A27185
A:Molecule type: mRNA
A:Residues: 1-626 <5A>
A:Cross-references: GB:X05301; MID:g56611; PIDN:CAA28920.1; PID:g56612
A:Stutcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E.

Cell 33, 671-682, 1983
 A:Title: Identifying the protein products of brain-specific genes with antibodies to
 A:Reference number: A90836; MUID:8329254; PMID:6347394

A:Accession: AY06356
A:Molecule type: mRNA
A:Residues: 7'KS, 3'11_626 <SUT>
A:Cross-references: GB:V01544; GB:J00756; NID:956879; PIDN:CAA24786.1; PID:9818027

A: Experimental source: clone pIB236
A: Note: the authors translated the codon CAG for residue 350 as Asn
R. Bloom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G.
J. Neurosci. 5, 1781-1802, 1985

A:Title: Immunocytochemical mapping of 18236, a brain-specific neuronal polypeptid
A:Reference number: 156564; MWID:85263773; PMID:4020419
A:Accession: 156564
A:Status: preliminary; translated from GR/FMR/MDP

A: Molecule type: mRNA
 A: Residues: KS_311-626 <RES>
 A: Cross references: GB:M6702; NID:9203181; PIDN:AAA40831.1; PID:9203182

A:Reference number: 152892; MUID:84206577; PMID:6586369

A:Accession: I52892
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'KS', 311-626 <RE2>

Comment: The sequence contains five presumably extracellular domains that are disulfide-linked. The long form predominantly in early postnatal life; alternative splicing of the gene produces a shorter form that is predominant in adult brain. At residues 100-101, the amino acid sequence is identical to that of the protein encoded by the *CDR1* gene.

C:\Genetics:	E:\Genetics
A\Gene:	MAG

A:Map position: 7
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
E:1-19/Domains: alternative splicing; brain; cell adhesion; duplication; glycoprotein; transmembrane
E:20-626/Product: myelin-associated glycoprotein, long splice form #status predicted <IG>
E:35-103/Domains: immunoglobulin homology <IM1>
E:118-120/Region: cell attachment (R-G-D) motif
E:153-219/Domains: immunoglobulin homology <IM2>
E:254-307/Domains: immunoglobulin homology <IM3>
E:340-394/Domains: immunoglobulin homology <IM4>
E:425-480/Domains: immunoglobulin homology <IM5>
E:514-536/Domains: transmembrane #status predicted <TM>
E:537-626/Domains: intracellular #status predicted <IN>
E:99,223,246,315,332,406,450,454/Binding site: carboxydrate (Asn) (Glycosyl) #status predicted

Query Match	10.9%	Score 295.5;	DB 1;	Length 626;
Best Local Similarity	22.2%	Pred. No. 1.4e-12;		
Matches 142;	Conservative 85;	Mismatches 235;	Indels 173;	Gaps 25;

[illegible]

RESULT 6
BNRT35
Myelin-associated glycoprotein precursor, short splice form - rat
N:Alternate names: 11236; brain neuron cytoplasmic protein 3; MAG
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
C:Accession: B29028; B27185; A60055
R:Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987

A:Title: Two forms of 18236/myelin-associated glycoprotein, a cell adhesion molecule
A:Reference number: A29028; MUID:87232001; PMID:2458699
A:Accession: B29028
A:Molecule type: mRNA
A:Residues: 1-582 <IIR>
A:Cross-references: GB:422357; NID:g205271; PIDN:AAA4158.1; PID:g205272
R:Salzer, J.L.; Holmes, W.P.; Colman, D.R.
J. Cell Biol. 104, 957-965, 1987
A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to
A:Reference number: A27185; MUID:87166195; PMID:2435742
A:Accession: B27185
A:Molecule type: mRNA
A:Residues: 419-582 <RNA>
A:Cross-references: GB:X06554; NID:g56614; PIDN:CAA29797.1; PID:g1334302
R:Tropk, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
Brain Res. 4, 143-155, 1988
A:Title: Differential splicing of MAG transcripts during CNS and PNS development.
A:Reference number: A60055

A:Accession: A60055
A:Molecule type: mRNA
A:Residues: 565-582 <TRO>
C:Comment: The sequence contains five presumably extracellular domains that are distributed in the adult and embryonic forms. The short form is found in the adult; the long form predominates in early C.elegans;
A:Gene: MAG
A:Map position: 7
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
K:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; tr F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-582/Product: myelin-associated glycoprotein, short splice form #status predicted F:35-102/Domain: immunoglobulin homology <IMM1>
F:118-120/Region: cell attachment (R-G-D) motif
F:152-219/Domain: immunoglobulin homology <IMM2>
F:254-307/Domain: immunoglobulin homology <IMM3>
F:340-394/Domain: immunoglobulin homology <IMM4>
F:425-490/Domain: immunoglobulin homology <IMM5>
F:514-536/Domain: transmembrane #status predicted <TM>
F:537-582/Domain: intracellular #status predicted <INT>
F:99, 223, 246, 315, 332, 406, 450, 454/Binding site: carbohydrate (ASX)
#status predicted

```

Query Match 10.7%; Score 269.5; DB 1; Length 582;
Best Local Similarity 23.2%; Pred. No. 3.3e-12;
Matches 110; Conservative 64; Mismatches 185; Indels 115; Gaps 14.

QY 21 FMIRVO-----ESVAVPEGLICITVSCSFSEYPRQDWTGSTRPAVGWYFKAVETET 68
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 10 FIMTISASRGHGMMGAMPSSISAFEGTQVSIICRRDFP--DDLRAVYVHGVIYFNSPIPK 67
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 69 KGAPATNHQSEVEYEMSTRGRQLTGDPAKGKCSLYIRDAOMODEOYEFVERGYSVYR 128
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 68 NTPVAFVFSRTQVWVHESFOGSRLLGDLGRNCTLLTETLSPELGKKYFFRDLGGYNOY 127
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 129 NEMNDGFLKATALOKPDVYIIPETLEGPQAPTVICVNNMAFECCP--PSPSMTGALS 186
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 128 TFESEH--SVLDITNTPNIVVPEPVAVAGTEVESCMP---DNCPELRPELMTWIGHGCL 180
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 187 SGGT-----KPTSHFSVLSTPPRODHTDTLCHVDFSRKGSQAORTVRLVAAYAP 238
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 181 GEPVTVLGRDEDEGTWQVSLHHPVPTREANGHRLGCQMAAPNTTLPREGYASLDVKRP 240
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 239 RDLVYSIS-----RDNTPPP-----PENRY-----259
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 241 VIVEMNSVEAIEGSHVSLGGAQSNRPPLLTMRDGNVLEAVALSITLDEEVTPAED 300
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 260 -----MNSQANRY-----LENIGNGTSLPYLEGOSLCLVYTHSSPPARLSW 302
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 301 GIYACLAENMAYGQDNRYELSVMYAPMKPTVNGVAVV--EGEYVSIICSTQSNDDPILTI 359
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 303 TQRQGVLSPSQDPDGLVELPRVOVEHEGDEPTCHARRPLDSQHSLSLWYHKGLISTA 362
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 360 FKREQILATVYESQDLELPRVATYTPBEDDGEVWCVAENQYQORATVNLVSFEAF-----413
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 363 FSNCAELGIGTIALFLPCLLA-----LIIMKLIPKRRTOETPRPFSSHSSTI 409
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```


Query Match 8.4%; Score 227; DB 2; length 862;
Best Local Similarity 21.7%; Pred. No. 1e-07;
Matches 97; Conservative 64; Mismatches 188; Indels 98; Gaps 16;

QY 5 LLLSLGSGQANDGRFW-IRVQESVAVPEGLCISVPCFS--YPRQDWTGSTPAYGYWF 61
DB 9 LLLGHNASQVSSANDWTVDPHDTLEAMEGACIRIPCKYKPLPKARLDNILLFQNYER 68
QY 62 KAVETTKGAPVATNHSREVESTGRFQLTGDPKAGCSLTIIRAQMODSQYFRRE 121
DB 69 DKATKKFKGT-VLYNAEPELPPKQRTYFLGN-SIDCKTLKIHPIRANSGNLGRMT 126
QY 122 RGSYVXKFNMDGFFLKVTALQKPDVYIPETLEPGQPTYICVN-----WAF 170
DB 127 AGT-----ERWMEPIHLNVSEKPPQYIQMSEIRESQVTLICGLNFSCFEYDILLQWFL 182
QY 171 EECPPPSFSWTAALSSQCKPPTSHF--SVLSFTPRPDHDTLCHVDSRKGVSAQR 228
DB 183 EDSKITSVTPSTSTSTSVTSISKNYTESKLTLPQPKWTDHCKSVKQVOHSSF-VLSER 241
QY 229 TVRLRYAVAP-----RDLVTSISRDNTPPDENLR 258
DB 242 TVRLDYKTYPKLEIKVNPTEVEKKNNSVTMTCRVNNSNPKLRTVAVSWFRDGRPLDQELE 301
QY 259 VAVSQANKTVL-----ENLNGTIS-----LPYLE 282
DB 302 -OEQMSKLLHLSVTKDMRKRCOASNDIGSEEEVELTVHVAPEPSRVHIYSPAE 360
QY 283 GOSLCLCVYTHSSPPA-RLSWQROQVLSPPSQPSD-PGVLELPRQVHEGEFTCHAHNP 340
DB 361 GGSVELICESLASPSNTNTWYHNKRP1---PGDTQELRIKVPSPWAGNYSCSLAENR 416
QY 341 LGSQHV--SLLSVHYKKGLISTAFSN 365
DB 417 LGHGKIDQEKADVHVAAPKAVTTVQS 443

RESULT 10
A:6512
CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: A46512
R:Torres, R.M.; Law, C.L.; Santos-Argumedo, L.; Kirihama, P.A.; Grabstein, K.; Parkhouse, J. Immunol. 149, 2641-2649, 1992
A:Title: Identification and characterization of the murine homologue of CD22, a B lymphocyte antigen.
A:Reference number: A46512; MUID:93017867; PMID:1401903
A:Accession: A46512
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-868 <TOR>
A:Experimental source: B cell lymphoma 38C13
A>Note: sequence extracted from NCBI backbone (NCBIRP:116156)

Query Match 8.1%; Score 220.5; DB 2; length 868;
Best Local Similarity 21.7%; Pred. No. 2.8e-07;
Matches 92; Conservative 57; Mismatches 173; Indels 101; Gaps 15;

QY 33 EGLCISVPCFS--YPRQDWTGSTPAYGYWFKAVETTKG-----AFVATNHSREVEMS 85
DB 38 EGACIRIPCKYKPLPKARLDNILLFQNYERDKATKKFTGTCLYLNKTEKDESELYXS 97
QY 86 TRGRFQLTGDPKAGCSLTIIRAQMODSQYFRVERGVYRNEMNDGFFLKVTALQK 145
DB 98 KQGVNTPLEGNRI-DNCTLKIHPIRANSGNLGRMTAGT-----ERWMEPIHLNVSEKPPQ 152
QY 146 PDVYIPETLEPGQPTYICVN-----WAFEECPSPFSWTAALSSQCKPPT 194
DB 153 PYIQMPEIRESQVTLICGLNFSCGYDILLKWFLEDSITTSVTSSTSVSSIK 212
QY 195 SHF--SVLSFTPRPDHDTLCHVDSRKGVSAQRTVRLRYAVAP----- 238
DB 213 NVYTESKLTLPQPKWTDHCKSVKQVOHSSK-VLSECTVHLDVYKTPKLEIKVNPTEVEKN 271

QY 239 -----RDLVTSISRDNTPPDENLRVAVSQANKTVL----- 269
DB 272 NSVWTMTCRVNNSNPKLRTVAVSWFRDGRPLDQELE-OEQMSKLLHLSVTKDMRGKRYC 330
QY 270 -----ENLNGTIS-----LPYLEGOSLCLCVYTHSSPPA-RLSWTOR 305
DB 331 QASNDIGFGESEEEVELTVHVAPEPSRVHIYSPAEQGSVELICESLASPSATVYTWYHN 390
QY 306 GQVLSPPSQPSD-PGVLELPRQVHEGEFTCHAHNPQSGHV--SLLSVHYKKGLISTA 362
DB 391 RKPI---PGDTQELRIKVPSPWAGNYSCSLAENRIGHGKIDQEKADVHVAAPKAVTV 446
QY 363 FSN 365
DB 447 IQS 449

RESULT 11
A:35648
B-cell adhesion protein CD22 alpha splice form precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C:Accession: A35648
R:Stamenkovic, I.; Seed, B.
Nature 345, 74-77, 1990
A:Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion.
A:Reference number: A35648; MUID:90231465; PMID:1691828
A:Accession: A35648
A:Molecule type: mRNA
A:Residues: 1-647 <STRA>
A:Cross-references: GB:X52785; NID:929778; PIDN:CAA36988.1; PID:929779
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
C:Superfamily: immunoglobulin homology
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transmembrane; signal sequence
F:1-19/Domain: extracellular #status predicted <SIG>
F:20-510/Domain: extracellular #status predicted <EXT>
F:432-484/Domain: immunoglobulin homology <IMM>
F:511-529/Domain: transmembrane #status predicted <TM>
F:530-647/Domain: intracellular #status predicted <CYT>
F:67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent)

Query Match 7.6%; Score 206.5; DB 2; length 647;
Best Local Similarity 19.0%; Pred. No. 1.8e-06;
Matches 130; Conservative 87; Mismatches 212; Indels 257; Gaps 27;

QY 1 MLPLLLSLGSGQANDGRFWI-IRVQESVAVPEGLCISVPCFS-----YPRQ 48
DB 3 LGGPMLLLVLELAFSDSSKWFEPETLYIMEGACVAPICPYRALDGLDLEFTLFPNP 62
QY 49 DWTGSTPAYGYWFKAVETTKGAPVATNHSREVESTGRFQLTGDPKAGCSLTIIRA 108
DB 63 EYKKNKSKPD--GTRLYESTKDGKVP-----SEQKRVQPLGDKKK-NCTLSHPV 109
QY 109 QMODSQYFRVERGVYRNEMNDGFFLKVTALQKPDVYIPETLEPGQPTYICVN- 167
DB 110 HLNDSQGLKRMES--KTERWMEPIHLNVSERPPIQDLPPIQESQEVTLTCLNF 165
QY 168 -----WAFEECPSPFSWTAALSSQGT-----KPTSHS SVLSFTPRPDH 209
DB 166 SCGYPIQIQWMLLEGVPMQAAVSTSLIKSVFTRSEKSPQSMHGGK-VTCQLODA 224
QY 210 D-----TDLTCHVDSRKGV----- 224
DB 225 DCKFLSNDTVQLNVKHPKAVTVYIQNPMPDIREGDTVLSQVNSNPSVRYEMKPKGA 284
QY 225 -----SAQRTVRLRYAVAPRD----- 241
DB 285 WEPSLGVULKIQNGWDMNTTACACNSWCSWASFPALNVQYADPDVAVRKIKPLSEIHS 344

QY 242 --VISISRONTDPDP-----ENLRVNVSA-----NRVLENT 272
 DB 345 GNSVSLQCDFFSSSHPEKVOEFMEKNGRLGKEQNLNDSISPEDAGSYSCWVNNISIGTA 404
 QY 273 GNGTSLPVL-----EGOSLICYVTHSSPPAR-----LSMTORGVLSP 311
 DB 405 SKAMTLEVLXAPRRRLRVNSPGDQVMEGKSATLTCSDANPPSHYTWDWNO----- 458
 QY 312 SOPSDGVLELPRVQVEHEGEFTCHARNHPLGSOHVSLS-LSVHYKKGLISTAFSNGAFGL 370
 DB 459 SLPLYSOKRLRELVKQVHSGAVWCQGTNSVKGKRSPLSLTLTYYSPETI-----GRRA 512
 QY 371 IGTALLFLCALIILIKI-----LPRK-RTQETPPRRSRHSTLIIDYINNVFTAGPLAQ 424
 DB 513 VEGGS-----CLALLILAIGLKLQRKWRKTSOQLOENS-----SCQSEF 554
 QY 425 KRQKATPNSPRTPLPGAPSPESKKKKQKQVLPSPFPKSTQAPESQSEQLHYAT 484
 DB 555 VRKKKVR-----RAPLSEG-----PHSLGCT-----NPMMDGISYTT 587
 QY 485 LNFPGVRRPREARMPKGTQADYAEVK 510
 DB 588 LRF-----PEMNIPRTGDAESSEMQ 607

RESULT 12

JH0371
 B-cell adhesion protein CD22 beta splice form precursor - human
 N:Alternate names: B-cell membrane protein CD22
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-2000
 C:Accession: JH0371; 156171
 R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
 J. Exp. Med. 173, 137-146, 1991
 A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
 A:Reference number: JH0371; MUID:91086838; PMID:1985119
 A:Accession: JH0371
 A:Molecule type: mRNA
 A:Residues: 1-847 <MIL2>
 A:Cross-references: GB:X59350; NID:q36090; PIDN:CAA42006.1; PID:q36091
 A:Experimental source: B lymphocyte
 A>Note: the authors translated the codon AAT for residue 358 as Met
 R:Wilson, G.L.; Naefeld, V.; Kozlow, E.; Menninger, J.J.; Ward, D.; Kehrl, J.H.
 J. Immunol. 150, 5013-5024, 1993
 A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
 A:Reference number: 156171; MUID:93267103; PMID:8496602
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <MIL2>
 A:Cross-references: GB:S61375; NID:q385980; PIDN:AAC18956.1; PID:q3184492
 C:Genetics:
 A:Gene: GDB:CD22
 A:Cross-references: GDB:127545; OMIM:107266
 A:Map position: 19q13.1-19q13.1
 A:Insertions: 138/1; 240/1; 359/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
 C:Superfamily: Immunoglobulin homology
 C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <NAT>
 F:346-398/Domain: Immunoglobulin homology <IMM1>
 F:609-661/Domain: Immunoglobulin homology <IMM2>
 F:668-706/Domain: transmembrane #status predicted <TRA>
 F:67-101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
 F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.5%; Score 202.5; DB 2; Length 847;
 Best Local Similarity 21.0%; Pred. No. 4.7e-06;
 Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;
 DB 1 MLPLLLSLGSGQAMDERFWI-RVQESVNVPEGICISVPCFS-----YPRQ 48
 3 LIGPWLILVLEYLAFSSDKSWFEPHETLYAWEGACWIPCTYRALDGLSEFTLEFHP 62

QY 49 DWTGSTPAYGWYKAVETTTKGAPVATNHQSRREVENSTREGQLTGDPAKNGSLYIRDA 108
 DB 63 EYKNKTSKPD-CTRLYESHKKQKVD-----SEQRKVGFLDKNK-NCTLSIHVP 109
 QY 109 QMODESQYFFRVERGSGYVRNFENNDGFELKVTALTKRPDYIPETLEPGQVTVICFN- 167
 DB 110 HLNDSQLGLRMS-----KTEKMERIHNLNVSRRPPPHIOLPPEIOESQVTLTGLNPF 165
 QY 168 -----WAECECPPSFSWTAALSSQGRKPTTSHPSVLSFTPRQDHTDLCYH 217
 DB 166 SCYGYPIQLQMLLEGVPMROAAVTSLSL-----TIKSVFRSELKSPQSHCKIYTCQL 221
 QY 218 -DFSRKGS-----AQRVLRVAYAPRDLYI-----SISRONTDPDP----- 255
 DB 222 QDADGKFLSNDYVOLNVKHTPKLEIKVTPSDALIVRGDSVYTMCEVSSSN-----PEYTV 277
 QY 256 -----NLR-VAVSQRN-----TVLENLNGTS----- 277
 DB 278 SWLKDTSLKQNTFTLNLREYVKDQSKYCCQVSDVGRSEEVFLQVYAPESPVO 337
 QY 278 ---LPVLEGOSLCTVCTHSSP-PARLSMTORGQVLSQSPDGVLELPRVQVEHEGEF 333
 DB 338 ILHSPAVESQVQVFLCMSLANPLPTNYTWYHNKEM---QGRTEEKVHPIKILPMHAGTY 394
 QY 334 TCHARRPLGS--QHVSLSLSVHYKKGLISTAFSNGAFGLIGITAL 377
 DB 395 SCVAENILGTGQRCGAEIDVGYPRKVTYIGNPMPIREGDVTVL 440

RESULT 13

A32164
 biliary glycoprotein 1 precursor, splice form a - human
 N:Alternate names: transmembrane carcinoembryonic antigen 1 (TMI-CEA); transmembrane
 C:Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice for
 C:Species: Homo sapiens (man)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
 R:Hindoa, Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wegener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
 A:Reference number: A32164
 A:Contents: erratum
 A:Accession: A32164
 A:Molecule type: mRNA
 A:Residues: 1-526 <HIN>
 A:Cross-references: GB:J03858; NID:q179439; PIDN:AAA51826.1; PID:q179440
 R:Hindoa, Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wegener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
 A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure
 A:Reference number: A94206; MUID:88320555; PMID:2457922
 A:Contents: annotation
 A>Note: the sequence shown in this reference has been completely corrected in referen
 R:Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elling, J.J
 J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mR
 A:Reference number: A92752; MUID:89139550; PMID:2537311
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <BAR1>
 A:Cross-references: EMBL:X16354; NID:q37197; PIDN:CAA34404.1; PID:q37198; EMBL:X14784
 A:Experimental source: splice form a
 A:Accession: B30127
 A:Molecule type: mRNA
 A:Residues: 1-319, 'D', 417-526 <BAR2>
 A:Cross-references: EMBL:X14831; NID:q37199; PIDN:CAA32940.1; PID:q37200; EMBL:X14784
 A:Experimental source: splice form b
 R:Barnett, T.R.; Drake, L.; Pickle IT, W.
 Mol. Cell. Biol. 13, 1273-1282, 1993
 A:Title: Human biliary glycoprotein gene: characterization of a family of novel alter
 A:Reference number: A48078; MUID:93140765; PMID:8423792
 A:Accession: A48078
 A:Molecule type: mRNA
 A:Residues: 124-141, 'H', 417-526 <BAR3>

A:Cross-references: GB:M76742; NID:g179480; PIDN:AA57142.1; PID:g179481
 A:Experimental source: splice form x
 A>Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:P123606)
 R:Hauck, W.; Nedeliec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
 Eur. J. Biochem. 223, 529-541, 1994
 A>Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami
 A:Reference number: S45664; MUID:9433343; PMID:8055923
 A:Accession: S45664
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <HAD>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 R:Nedeliec, P.; Turbide, C.; Beauchemin, N.
 Eur. J. Biochem. 231, 104-114, 1995
 A>Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
 A:Reference number: S65939; MUID:95354678; PMID:7628460
 A:Accession: S65939
 A:Status: Preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-21 <NED>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A>Title: Identification of three new genes and estimation of the size of the carcinoemb
 A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Contents: annotation; alignment of related sequences
 A:Gene: GDB:BCP
 A:Cross-references: GDB:127992; OMIM:109770
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MA7A>
 F:35-428/Domain: extracellular #status predicted <EXT>
 F:35-319, 'D', 417-526/Product: biliary glycoprotein 1, splice form b #status predicted <F
 F:35-141, 'H', 417-526/Product: biliary glycoprotein 1, splice form x #status predicted <F
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>
 F:341-398/Domain: immunoglobulin homology <IMM3>
 F:425-454/Domain: transmembrane #status predicted <TM4>
 F:453-526/Domain: intracellular #status predicted <INT>
 F:104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405, 475/34

Query Match 6.9%; Score 186; DB 1; Length 526;
 Best Local Similarity 21.5%; Pred. No. 3, 5e-05;
 Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31;

QY 5 LLLSLGGSGAMGRVIRVQESVWVEGICISVP-----CSFSYPRQDWTGSPAY 57
 DB 19 LLLSLSL-----TWNPPTTAQLTTESMPENVAEGEYLLVHNLPGQ-----LF 63
 QY 58 GY-WFKAVETTKGAPVATNHSREVMSTRGRQLGDPKAG-----NCSLVTRDAQ 109
 DB 64 GYSWYKG--ERYDG-----NQIVGAIIGTQQAIPGANSRGRETIYNASLLIONVT 113
 QY 110 MDESQYFFRVERGSYVRFMDGFLKVTALTKPDVYIPETLEEGQPVTVICVFNMA 169
 DB 114 QNDGFTYLOV-----IKSDLVNE-----EATGQHVY----- 141
 QY 170 FEEDPPPSFWTGAALSSQGTPTTSHFVSLSTPRPDHDTDLCHVDFSRKVSQAQRT 229
 DB 142 -PELPKPS-----ISSNSNPVEDKDAV-AFTCEPETDITTYLWMINOSLP----- 189
 QY 230 VRLVAVAPRDL-VISISPDNTPDPENLRFVAVSOANRT--VLENGNGSLPVL----- 282
 DB 190 -RLQISGNRTLLTLLSTRNDGPRCEIIONPVS-ANRSDPYTLNVTYGGDTPTTISPSDT 247
 QY 283 -----GOSLCLVCTHSSPAPRLSWTORGQVLSPOPSDQVLELPRVQVHEGEFTCHAR 338

DB 248 YRRPANLSLSCYASNPDAQSWLINFPGQSTGE-----LFIPIVNNSGSTYCAN 302
 QY 339 HPL-GSHVSLSLSHYHKKGLISTAFS-----NGAFIGITALLFLCLA 382
 DB 303 NSVTCNKRIV-----KTIIVELSPVAKPOIKASKTIVTGKDSVNL-----CST 350
 QY 383 L---IMKILPKRRRTQTEPPRFRSHSTIIDIYINV-----TAGP 421
 DB 351 NDTGISIMFKNQSLPSSERKMLSGQNTTIS-INPKAREDACTYWEVFNPIKNSDP 409
 QY 422 LAQKNOKATPNSPRTPLPGA-----PSPESKKN 451
 DB 410 IMLNPNVALPO--ENGSLPGAIGIVVALVALVALACFLHFGKTRASDQGRDLT 467
 QY 452 QKQYOLPSPPEKPSSTO--APESQSEELHATLNFPGVRP-RPARMPK--GTQADY 506
 DB 468 EHK-----PVSNNHODHSNDPPKNKEVYISTLNEAQQPOTPSASPSLTATETIY 520
 QY 507 AEVKFRQ 512
 DB 521 SEVRKQ 526

RESULT 14

T09062
 Probable advanced glycosylation end-products receptor precursor - mouse
 N:Alternate names: RAGE
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;
 submitted to the EMBL Data Library, October 1997
 A:Description: Sequence of the mouse major histocompatibility locus III region.
 A:Reference number: Z16543
 A:Accession: T09062
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-402 <ROW>
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950
 C:Gene: RAGE
 A:Map position: 17
 A:Intons: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
 C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
 C:Keywords: receptor; transmembrane protein
 F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 184; DB 2; Length 402;
 Best Local Similarity 23.4%; Pred. No. 3, 4e-05;
 Matches 101; Conservative 46; Mismatches 139; Indels 146; Gaps 20;

QY 100 NCSLVIRDAQMDQESYFFRV--EKGSYRYFMNDGFLKVTALTKPDVYIPT-LEP 156
 DB 80 NSLLLPATGIVDEGFRKATNRGKEKVSRYR-----VRVYQIIPGRPEIYDPASETLA 134
 QY 157 GQPVTV-ICVFWMAFECPSPFSW--TGAALSSQGT-----PTSHESVLS-F 202
 DB 135 SVPNKKGIVCGSGSY---PAGLSWHMLDCKLLIPGKETLYKEETRRRPETGLTIRSEL 191
 QY 203 TRPDHDTDLCHVDFSKKVSQAQTVKRLVAVAPRDLVISISDNTPPDENLRFVWS 262
 DB 192 TVIPIQGQHTPFSQSF-S-IGIPRRRRPLNT---APIQ-----RVRRPPEGIGQLLVE 241
 QY 263 QANRTVLENLGNGTSLPVLEGOSLCLVCYTHSSPARLSWTRQGVLSPOPSDQVLEL 322
 DB 242 PEGCI-----VAPGETVTLTCAISQPPQVWMKDGAPL-PLAPSP--VLLL 286
 QY 323 PRVQVHEGEFTCHARHPLGSHVSLSLSHY-----KKGLISTAFSNGAF 368
 DB 287 PEVGHEDGTYSCVATHPSSHQPSRPYSINVTETGDEGPAEGSGEGSLTALALAGIL 346
 QY 369 LGIGITALLFLCLALIMKILPKRRRTQTEPPRFRSHSTIIDIYINVPTAGPLAQRNQ 428

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Db      347 GGLGVALL-----||:|:|:|-----||:|:|:|-----VGLALMKRRQ 365
Oy      429 KATPNSPRTPLPCAPSPESKKNOKOYOLPSPPEPKSSTOAPESQSEQLHYATINFP 488
Db      366 -----||:|:|-----PREPERK-----APESQDEEB--RAELN-- 387
Oy      489 GVRPRPAPRMPK 500
Db      388 ---QSEEREMPE 396

RESULT 15
A:Accession: A38096
A:Reference number: A38096; MUID:92235084; PMID:1569102
A:Title: Primary structure of the human heparan sulfate proteoglycan from basement mem-
tor, laminin, neutral cell adhesion molecules, and epidermal growth factor.
A:Accession: A38096
A:Molecule type: mRNA
A:Residues: 1-4391 <MUR>
A:Cross-references: GB:MB5289; NID:g184426; PID:AAA52700.1; PID:g184427
R:Kallunki, P.; Trygvason, K.
J. Cell Biol. 116, 359-571, 1992
A:Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro-
ell adhesion molecules, and epidermal growth factor.
A:Reference number: A41736; MUID:92112994; PMID:1730768
A:Accession: S19256
A:Molecule type: mRNA
A:Residues: 1-57, 'D', '59-434, 'A', '436, 'FL', '438-449, 'Q', '451-502, 'A', '503-792, 'K', '794-908, 'R',
71-2979, 'H', '2981-2994, 'G', '2996-3167, 'T', '3169-3240, 'R', '3242-3426, 'R', '3428-3631, 'Q', '3633-3
A:Cross-references: EMBL:X62515; NID:g29469; PID:CAA44373.1; PID:g29470
R:Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Trygvason, K.
Genomics 11, 389-396, 1991
A:Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g
A:Reference number: A41059; MUID:92120660; PMID:1685141
A:Accession: A41059
A:Molecule type: mRNA
A:Residues: 'RT', '892-908, 'R', '910-1101, 'L', '1103-1132, 'L', '1134-1223-1397 <KA2>
A:Cross-references: GB:S6436; NID:g243370; PID:AA821121.1; PID:g243371
J. Dodge, G.R.; Kovalevsky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo,
Genomics 10, 673-680, 1991
A:Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula
A:Reference number: A40306; MUID:91365376; PMID:1679749
A:Accession: A40306
A:Molecule type: mRNA
A:Residues: 1018-1405, 'G', '1407-1409, 'G', '1411-1465 <DDO>
A:Cross-references: GB:MK4283; NID:g184424; PID:AAA52699.1; PID:g184425
R:Heemann, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 109, 3199-3211, 1989
A:Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
anes.
A:Reference number: A33625; MUID:90078352; PMID:2687294
A:Accession: B33625
A:Molecule type: protein
A:Residues: 1379-1384, 'X', '1386-1388, 'X', '1390-1398 <HE2>
A:Accession: A33625
A:Molecule type: protein
A:Residues: 2166-2171, 'X', '2173-2175, 'X', '2177-2185 <HE3>
A:Residues: 2166-2171, 'X', '2173-2175, 'X', '2177-2185 <HE3>

```

A>Note: peptide potentially matches four different regions of sequence shown

C:Genetics:

A:Gene: GDB:HSPG2

A:Cross-references: GDB:126372; OMIM:142461

A:Map position: 1p36.1-1p36.1

C:Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G ;

C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmem

F:1-21/Domains: signal sequence #status predicted <SIG>

F:12-4391/Product: perlecan #status predicted <MAT>

F:12-193/Domains: I <DOM1>

F:194-530/Domains: II <DOM2>

F:199-234/Domains: LDL receptor ligand-binding repeat homology <LDL1>

F:285-339/Domains: LDL receptor ligand-binding repeat homology <LDL2>

F:325-359/Domains: LDL receptor ligand-binding repeat homology <LDL3>

F:368-403/Domains: LDL receptor ligand-binding repeat homology <LDL4>

F:531-1676/Domains: III <DOM3>

F:1159-1206/Domains: laminin-type EGF-like homology <LEG>

F:1563-1610/Domains: laminin-type EGF-like homology <EGT>

F:1613-1668/Domains: laminin-type EGF-like homology <LEB8>

F:1677-3686/Domains: IV <DOM4>

F:2007-2034/Domains: transmembrane #status predicted <TRM>

F:3687-4391/Domains: V <DOM5>

F:3845-3880/Domains: EGF homology <EGF1>

F:3888-3921/Domains: EGF homology <EGF>

F:3993-4106/Domains: laminin G repeat homology <LG2>

F:4147-4175/Domains: EGF homology <EGF2>

F:4149-4151/Region: motor neuron attachment (L-R-E) motif

F:4299-4301/Region: motor neuron attachment (L-R-E) motif

F:657-7176/Binding site: heparan sulfate (Ser) (covalent) #status predicted

F:89-554,1155,2121,3072,3105,3279,3780,3936,4068/Binding site: carbohydrate (asn) (co

F:2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 6.7%; Score 180; DB 2; Length 4391;

Best Local Similarity 20.4%; Pred. No. 0.0013;

Matches 129; Conservative 68; Mismatches 214; Indels 222; Gaps 30;

QY 18 DGRWIRQVESVMPEGLICISVPCSFSPROD--WT--GSTPA-----YGVW----- 60

Db 3119 EGPVWVKVKAATLE--CVSA---GPRSSAKMTIRISSVPALKLEQTYLMDSHAVIQ 3171

QY 61 -----FAAVETTKGAPVATNHDSREVENSTRG----- 88

Db 3172 ISSAKPDSAGTYVCLAONALCTAOKQVEVIVDTGAMAGAPQVQAEELVLEGHATYL 3231

QY 89 RFOLTGDA-----KGNCSLYIRDAQMDQESQFFRVERGYSVRYNF 130

Db 3232 RGSATGSAPIRTHMSKLSRLPMQHRLEGDLILIRVAQ-QDSQYI-----CNA 3280

QY 131 MNDFELKVVAL--TQKPD--VYIPE--TLEPGQVTVICVENNAFEECPSPFSWGA 184

Db 3281 TSPAGHAETATILIHVESPPYATVPEHSAVOAGETVLOCLAHGT---PLTLQWMSRVG 3336

QY 185 LSSOGTKTTHFSVLSSTPRPDHDDTLCHVDPSKRGVSAQKTVLRVAYARDL-VI 243

Db 3337 SSLPGR--ATARNELHFERAAPEDSGRYKRV--TKNVGSALEAFADLVLVGPGSLPAT 3392

QY 244 SISRDNPDPENLRVMSQANRRVLELNGTSLPYE-----GSLCLTVCTHSSPPAR 299

Db 3393 SIPIAGSTP-----TVQVT-----POLETSTIGASVEFHCAVPSDQCTQ 3430

QY 300 LSWTQRGVLSPPSPDGVLELPRVOVEHEGEFTCAHRLPSQHWLSLSVYKGLI 359

Db 3431 LRWKEGGQLPRPHSGVDQGVLRIONLDQSCGQYICQAHGPMGKAQASQAVIQAIPSVL 3490

QY 360 STAFSNGAFGLGIGTALLFLCLALIMKILPKRKRTQFTTPRRS----- 404

Db 3491 INPIRVSQTVVVG--HAVEFECLAL-----GDPKPOVTWMSKVGHLPRIQVS 3536

QY 405 -----RSTLID-----YINVPYTAGP-----LAOKRANKATPNSPRTP----- 438

Db 3537 GGAVRIAHVELADAGQYRCTYTNAGTITQSHVILLVQAALPDISMPQEVRYVAGSAAVAPC 3596

QY 439 LPPGAPSPESKRNKKQYQVLPSPPEPKSSTQAPESQESQEBLAVATINFGVRR----- 493

Thu Oct 9 09:53:38 2003

us-09-937-636-3.rpr

Page 10

Db	3597	IASGYPTPDISWS-KIDGSLP-----PDSR-----LENNMLLPVVRPDAGTY	3639
OY	494	-----PEARMPKGTQADYA	507
Db	3640	VCTATNRQKVKAF AHLQVPERVVPYFTQTPYS	3672

Search completed: October 8, 2003, 20:04:14
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 19:40:42 ; Search time 18 Seconds
(without alignments)
1337.648 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706
Sequence: 1 MLLPLLSLGLGSGQMDGR.....RPEARMPKGTQADYAEVKRQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2576.5	95.2	697	1	SILA_HUMAN
2	1513.5	55.9	686	1	SILE_HUMAN
3	947	35.0	499	1	SILH_HUMAN
4	909	33.6	595	1	SILH_HUMAN
5	909	33.6	597	1	SILH_PANTR
6	873	32.3	467	1	SILH_MOUSE
7	870	32.2	463	1	SILH_HUMAN
8	836	30.9	442	1	SILH_HUMAN
9	832.5	30.8	467	1	SILH_HUMAN
10	804.5	29.7	551	1	SILS_HUMAN
11	694	25.6	364	1	CD23_HUMAN
12	689.5	25.5	569	1	SILF_MOUSE
13	528	19.5	403	1	CD33_MOUSE
14	303.5	11.2	626	1	MAG_HUMAN
15	302.5	11.2	620	1	SMP_COTJA
16	295.5	10.9	626	1	MAG_RAT
17	288.5	10.7	626	1	MAG_MOUSE
18	268	9.9	1709	1	SN_HUMAN
19	245	9.1	1694	1	SN_MOUSE
20	227	8.4	862	1	CD22_MOUSE
21	202.5	7.5	847	1	CD22_HUMAN
22	198	7.3	330	1	CD22_PONPY
23	193.5	7.2	332	1	CD22_PANPA
24	193.5	7.2	332	1	CD22_PANTR
25	186	6.9	526	1	CEAL_HUMAN
26	179	6.6	402	1	RAGE_RAT
27	179	6.6	4391	1	PGBM_HUMAN
28	176	6.5	332	1	CD22_GORGO
29	175.5	6.5	1234	1	NPHN_RAT
30	172.5	6.4	403	1	RAGE_MOUSE
31	161.5	6.0	1242	1	NPHN_MOUSE
32	158	5.8	335	1	PSG2_HUMAN
33	155	5.7	3707	1	PGBM_MOUSE

34	153.5	5.7	416	1	RAGE_BOVIN	028173 bos taurus
35	151.5	5.6	1241	1	NPHN_HUMAN	060500 homo sapien
36	147.5	5.5	1906	1	KML5_CHICK	P11799 gallus gall
37	143	5.3	702	1	CEAL_HUMAN	P06731 homo sapien
38	142.5	5.3	417	1	PVR_HUMAN	P15131 homo sapien
39	141.5	5.2	739	1	VCAI_MOUSE	P29533 mus musculu
40	140.5	5.2	428	1	PSG3_HUMAN	P16557 homo sapien
41	140	5.2	628	1	LU_HUMAN	P50895 homo sapien
42	139.5	5.2	419	1	PSG7_HUMAN	P13046 homo sapien
43	139	5.1	404	1	RAGE_HUMAN	P15109 homo sapien
44	138.5	5.1	349	1	CEAL_HUMAN	P31997 homo sapien
45	137	5.1	521	1	CEAL_MOUSE	P31809 mus musculu

ALIGNMENTS

RESULT 1	ID	SILA_HUMAN	STANDARD:	PRT:	697 AA.
AC	096LC7	096G54	096LC8		
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Stalle acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2).				
GN	SIGLEC10 OR SIG2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RX	MEDLINE-21303047; PubMed-11409878;				
RA	Yousaf G.M., Odon M.H., Fousias G., Diamandis E.P.;				
RT	Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SIG2) with three splice variants.";				
RL	Biochem. Biophys. Res. Commun. 284:900-910(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE-Spleen;				
RX	MEDLINE-21181584; PubMed-11284738;				
RA	Floyd J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G.,				
RT	Munday H., Matiel M.-G., Moore P., Liu D., Crocker P.R.;				
RL	"Identification, characterization and leucocyte expression of Siglec-10, a novel human stalle acid-binding receptor.";				
RN	Biochem. J. 355:489-497(2001).				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE-Dendritic cell;				
RA	MEDLINE-21359381; PubMed-11358961;				
RT	Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;				
RL	Cloning and characterization of Siglec-10, a novel stalle acid binding member of the Ig superfamily, from human dendritic cells.";				
RN	J. Biol. Chem. 276:28106-28112(2001).				
RP	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.				
RX	MEDLINE-22152890; PubMed-12163025;				
RA	Kizig F., Martinez-Barriocanal A., Lopez-Bolet M., Sayos J.;				
RT	Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";				
RL	Biochem. Biophys. Res. Commun. 296:355-362(2002).				
RN	[5]				
RP	SEQUENCE OF 334-697 FROM N.A. (ISOFORM 1/3/4).				
RC	TISSUE-B-cell;				
RX	MEDLINE-22188257; PubMed-12477932;				
RA	Straussberg R.L., Felinold E.A., Grouse L.H., Derge J.G.,				
RT	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RL	Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RL	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttenfield Y.S.N., Krzywinski M.I., Skalska U., Smalms D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3- or
 CC 2,6-linked sialic acid. The sialic acid recognition site may be
 CC masked by cis interactions with sialic acids on the same cell
 CC surface. In the immune response, may act as an inhibitory receptor
 CC upon ligand induced tyrosine phosphorylation by recruiting
 CC cytoplasmic phosphatase(s) via their SH2 domain(s) that block
 CC signal transduction through dephosphorylation of signaling
 CC molecules.
 CC -1- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4);
 CC Secreted (isoform 5).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Long;
 CC IsoId-Q96LC7-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short, Sv1;
 CC IsoId-Q96LC7-2; Sequence=VSP_002565;
 CC Name=3; Synonyms=SV3;
 CC IsoId-Q96LC7-3; Sequence=VSP_002564;
 CC Name=4; Synonyms=SV4;
 CC IsoId-Q96LC7-4; Sequence=VSP_002561;
 CC Name=5; Synonyms=SV2;
 CC IsoId-Q96LC7-5; Sequence=VSP_002562, VSP_002563;
 CC -1- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
 CC (eosinophils, monocytes and a natural killer cell subpopulation).
 CC Isoform 5 is found to be the most abundant isoform. Found in lymph
 CC node, lung, ovary and appendix. Isoform 1 is found at high levels
 CC and isoform 2 at lower levels in bone marrow, spleen and spinal
 CC chord. Isoform 2 is also found in brain. Isoform 4 is specifically
 CC found in natural killer cells.
 CC -1- DOMAIN: contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the
 CC termination of the immune response. The phosphorylated ITIM motif
 CC binds to the SH2 domain of PTPN6/SHP-1.
 CC -1- PTM: Tyrosine-phosphorylated
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
 CC (SIALIC ACID BINDING IS-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -----
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 CC -----
 DR EMBL: AY029277; AAK40255.1; -
 DR EMBL: AY029277; AAK40256.1; -
 DR EMBL: AF310233; AAK55139.1; -
 DR EMBL: AF311905; AAK92542.1; -
 DR EMBL: AY032685; AAK51124.1; -
 DR EMBL: BC009955; AAH09955.1; -
 DR Genbank: HGNC:15620; SIGLEC10.
 DR MIM: 606091; -
 DR Interpro: IPR007110; Ig-1like.

DR Interpro: IPR003599; Ig.
 DR Interpro: IPR003598; Ig_C2.
 DR Interpro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00409; Ig; 4.
 DR SMART: SM00408; IgC2; 2.
 DR PROSITE: PS00835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Phosphorylation; Alternative splicing;
 KW Polymorphism.
 FT SIGNAL 1 16
 FT CHAIN 1 697
 FT DOMAIN 17 550
 FT TRANSMEM 551 571
 FT DOMAIN 572 697
 FT DOMAIN 18 121
 FT DOMAIN 146 231
 FT DOMAIN 251 339
 FT DOMAIN 344 441
 FT SITE 595 600
 FT SITE 665 670
 FT DISULFID 36 173
 FT DISULFID 41 101
 FT DISULFID 164 215
 FT DISULFID 276 323
 FT DISULFID 380 425
 FT MOD_RES 667 667
 FT CARBOHYD 100 100
 FT CARBOHYD 355 355
 FT CARBOHYD 364 364
 FT CARBOHYD 486 486
 FT CARBOHYD 504 504
 FT VARSPLIC 125 214
 FT VARSPLIC 140 185
 FT VARSPLIC 186 697
 FT VARSPLIC 141 198
 FT VARSPLIC 445 539
 FT MUTAGEN 667 667
 FT CONFLICT 28 28
 FT CONFLICT 134 134
 FT CONFLICT 226 226
 FT CONFLICT 334 336
 FT CONFLICT 344 344
 FT CONFLICT 440 440
 FT CONFLICT 587 587
 FT CONFLICT 625 625
 SQ SEQUENCE 697 AA; 76619 MW; 6CB231CE4911D1B CRC64;
 Query Match 95.2%; Score 2576.5; DB 1; Length 697;
 Best Local Similarity 73.0%; Pred. No. 1,8e-173;
 Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
 QY 1 MLPLLSLLSLGSGQAMDGRFWIRVOESYVWVEGLCTISVCSFSYPRODMTSPAYGW 60
 DB 1 MLPLLSLLSLGSGQAMDGRFWIRVOESYVWVEGLCTISVCSFSYPRODMTSPAYGW 60
 QY 61 FRAVETTTGAPVAINHOSREVEKSTRGFQLTGPANGCSLVIRDAQMDQESQYFFRV 120
 DB 61 FRAVETTTGAPVAINHOSREVEKSTRGFQLTGPANGCSLVIRDAQMDQESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFLKVTALTKRPDYIIPETLEPGQPVYVYCVNNAFECCPPSPSW 180
 DB 121 ERGSYVRYNFMNDGFLKVTALTKRPDYIIPETLEPGQPVYVYCVNNAFECCPPSPSW 180
 QY 121 ERGSYVRYNFMNDGFLKVTALTKRPDYIIPETLEPGQPVYVYCVNNAFECCPPSPSW 180
 DB 121 ERGSYVRYNFMNDGFLKVTALTKRPDYIIPETLEPGQPVYVYCVNNAFECCPPSPSW 180

QY	181	TGAA	SSGCTPTTSHFVSLSTPRPOHDITLCHVDSRKGVSAQRTVRLVAAAPD	240
Db	181	TGAA <th>SSGCTPTTSHFVSLSTPRPOHDITLCHVDSRKGVSAQRTVRLVAAAPD</th> <td>240</td>	SSGCTPTTSHFVSLSTPRPOHDITLCHVDSRKGVSAQRTVRLVAAAPD	240
QY	241	LVIS	RDNTD-----	252
Db	241	LVIS	RDNTALEPQPGQNNVYLEAKGQFLRLCADSDQPATLSWLQNRVSSHP	300
QY	253	-----	-----PPENLRMVSAQNRVYLE	270
Db	301	WGPR	LGLEPVGKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRMVSAQNRVYE	360
QY	271	NLGN	STLPYLEGOSGLCYCVTHSSPPARLSWTORGQVYSPQSPQGVLELPRVGEH	330
Db	361	NLGN	STLPYLEGOSGLCYCVTHSSPPARLSWTORGQVYSPQSPQGVLELPRVGEH	420
QY	331	GEFT	CHARHPGSGHVSLSLSVHY-----	354
Db	421	GEFT	CHARHPGSGHVSLSLSVHYSPKLLGPGSCWEAEGLHSCSSQASPARSLRWLGE	480
QY	355	-----	-----K	355
Db	481	ELLE	GNSSQDSFEVTPSSAGPWANSSLSLHGSLSGRLRCAMNHYGAQSGSITLDPDK	540
QY	356	KGLI	STARSNAGFLGIGITALLFLCALILIMLILPKRRTQTEPRPRFSRHSITLDYINV	415
Db	541	KGLI	STARSNAGFLGIGITALLFLCALILIMLILPKRRTQTEPRPRFSRHSITLDYINV	600
QY	416	VPTAG	PLAKQKNQKATPNSPRTPLPPGAPSPESKKNQKQOYLPSPEPKSSQAPESQ	475
Db	601	VPTAG	PLAKQKNQKATPNSPRTPLPPGAPSPESKKNQKQOYLPSPEPKSSQAPESQ	660
QY	476	SOEEL	VATLNPQVRPRPEARMKGTQADVAEVEFQ	512
Db	661	SOEEL	VATLNPQVRPRPEARMKGTQADVAEVEFQ	697

RESULT 2

ID	STLB_HUMAN	STANDARD:	PRT:	686 AA.
AC	Q6RLE6:			
DY	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Static acid binding Ig-like lectin 11 precursor (Siglec-11) (Static acid-binding lectin 11).			
GN	SIGLEC11.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND INTERACTION WITH PTPN6 AND PTPN11.			
RA	MEDLINE=22086217; PubMed=11986327;			
RT	Angela T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R., Varki A.;			
RT	"Cloning and characterization of human Siglec-11. A recently evolved signaling that can interact with SHP-1 and SHP-2 and is expressed by tissue macrophages, including brain microglia.";			
RL	J. Biol. Chem. 277:24466-24474(2002).			
CC	-1- FUNCTION: Putative adhesion molecule that mediates static-acid dependent binding to cells. Preferentially binds to alpha2,8-linked static acid. The static acid recognition site may be masked by cis interactions with static acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.			
CC	-1- SUBUNIT: Interacts with PTPN6/SHP-1 and PTPN11/SHP-2 upon phosphorylation.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- TISSUE SPECIFICITY: Expressed by macrophages in various tissues			

```
CC      including Kupffer cells. Also found in brain microglia.
CC      -1 DOMAIN: Contains an intracytoplasmic motif referred as
CC      immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
CC      is involved in downmodulation of cellular functions as the
CC      termination of the immune response.
CC      -1 PPM: Phosphorylated on tyrosine residues.
CC      -1 SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC      (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC      -1 SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -1 SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC      -----
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CC      or send an email to licensese@isb.sib.ch).
CC      -----
DR      EMBL; AF37818; AAK72907.1; -
DR      Genew; HGNC:15622; SIGLECI1.
DR      MIM: 607157; -
DR      InterPro; IPR007110; Ig_1like.
DR      InterPro; IPR003598; Ig_C2.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; Ig; 3.
DR      SMART; SMO0408; IGC2; 2.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW      Immunoglobulin domain; Repeat; Phosphorylation.
FT      SIGNAL          1         15
FT      CHAIN           16        686
FT      DOMAIN          16        549
FT      TRANSMEM       550       572
FT      DOMAIN          573        686
FT      DOMAIN          19        122
FT      DOMAIN          147        232
FT      DOMAIN          239        338
FT      DOMAIN          343        440
FT      SITE            630        635
FT      DISULFID        37        174
FT      DISULFID        42        102
FT      DISULFID        165        216
FT      DISULFID        275        322
FT      DISULFID        379        424
FT      CARBOHYD        43        443
FT      CARBOHYD        78        78
FT      CARBOHYD        250        250
FT      CARBOHYD        354        354
FT      CARBOHYD        363        363
FT      CARBOHYD        485        485
FT      CARBOHYD        503        503
SQ      SEQUENCE
      686 AA; 74544 MW; PDDEA193615E5A8 CRC64;

Query Match      55.9%; Score 1513.5; DB 1; Length 686;
Best Local Similarity 46.6%; Pred. No. 7.4e-99;
Matches 323; Conservative 51; Mismatches 102; Indels 217; Gaps 6;
```


Query Match 32.3%; Score 873; DB 1; Length 467;
 Best Local Similarity 38.9%; Pred. No. 4,2e-54;
 Matches 203; Conservative 74; Mismatches 171; Indels 74; Gaps 11;

QY 2 LPLLSLLGSGAMGR-----FWIRVOESVWPEGLCISVPCSESYPRQ---DWTGS 53
 Db 1 MLLLLLLLMGLKGVGQNPQVEFTLNVKRRKGLCVLPNCNFSYLKRLRLDWTGS 60

QY 54 TPAYGWFKAVTETTKAPVATNHNOSREVMSTRGRFOLGDAKNGCSIVTDAOMDE 113
 Db 61 DPVGFVREGTRBRKDSIVATNNPIKAKVETRNPFLLGDWRNDSINTIEIRKKA 120

QY 114 SQFFRERGRSRYRYNPMNDGFLLKATALTOKPDVYIPELTPEGPVYICVFNNAFEEC 173
 Db 121 GLTFEFLERGR-TRYNMMDKMTLVYALTNPQILLPELTLEAGHSNLTCSVPMDCGVT 179

QY 174 PPFSFWTGAALSSQGRKPTTSHFSVLSFPFRODDHDLTGVDSSKRGVSAQRTVLR 233
 Db 180 APPIFWMTGTSVFLSTNTGS--SVLTTPPODHTGMLTCQVTLPGTNVSTRMTTRLN 237

QY 234 VAPAPDLVYISIRDTPPPELNRVMSQANRTVLENNGTSLPVEGQSICLYCVTH 293
 Db 238 VSYAPK-----NLVTIVYQADSVSTILKNSSLPISGQSLRLICSTD 281

QY 294 SSPARLMTQRGQVLSPOSPDGYLEPRQVEHEGFTCHARRPLGSHVSLSVH 353
 Db 282 STPPALMSWMDNLTLCPKSLKPGLEFPVHLKGVGYTQAOAHALGSHISLSLSPQ 341

QY 354 YKGLISTAFSNGAFGLGITALLFLCLALIMKILPKRRQTE---TPRFRSRHSTI 409
 Db 342 SSATL--SEMMMGTEFGSCVTLALLFVLCILLAVRSYRKARAVAPNRP----- 391

QY 410 LRYINVPYAGLAKRKNKATPNRPPLPGADSPESKKNOKKOYLPSFPEKKSSTO 469
 Db 392 -DALKVSQNPVLSQADS-----SEPLSILEA 421

QY 470 APEQSQDELHYATLNFPGVRRPEARNPKGTADYEVKR 511
 Db 422 ABSSTE--EELHYATLSHEMKPM-NLMGQDDTTEYSLEIKF 460

RESULT 7
 SILE_HUMAN
 ID SILE_HUMAN STANDARD; PRT; 463 AA.
 AC Q9Y336; Q9BY19;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sialic acid-binding Ig-like lectin 9 precursor (Siglec-9) (FOAP-9 protein).
 GN SIGLEC9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=2036134; PubMed=10903843;
 RA Fousias G., Yousef G.M., Diamandis E.P.;
 RT "Identification and molecular characterization of a novel member of
 the siglec family (SIGLEC9).";
 RL Genomics 67:171-178(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone marrow;
 RX MEDLINE=20357333; PubMed=10801862;
 RA Zhang J.Q., Nicoll G., Jones C., Crocker P.R.;
 RT "Siglec-9, a novel sialic acid binding member of the immunoglobulin
 superfamily expressed broadly on human blood leukocytes.";
 RL J. Biol. Chem. 275:22121-22126(2000).
 RN [3]
 RP SEQUENCE FROM N.A. AND MUTAGENESIS OF ARG-120.
 RC TISSUE=Peripheral blood;

RX MEDLINE=20357334; PubMed=10801860;
 RA Angata T., Varki A.;
 RT "Cloning, characterization, and phylogenetic analysis of siglec-9, a
 RT new member of the CD33-related group of siglecs. Evidence for
 RT co-evolution with sialic acid synthesis pathways.";
 RL J. Biol. Chem. 275:22127-22135(2000).
 RN [4]
 RP SEQUENCE FROM N.A. AND VARIANT GLU-315.
 RA Takayama K., Fujii Y., Turtutan K., Kawaguchi A., Ukai Y.,
 RA Ametia C., Yajima Y., Yazaki M.;
 RT "Molecular cloning of a novel gene, FOAP-9, which are induced by
 RT oxidized LDL in human macrophages";
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillgen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Dangnan L., Ertler A., Christensen M., Georgesou A., Avila J., Liu S.,
 RA Andrade S., Trankheim M., Altix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3- or
 CC 2,6-linked sialic acid. The sialic acid recognition site may be
 CC masked by cis interactions with sialic acids on the same cell
 CC surface.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
 CC (neutrophils and monocytes but not eosinophils). Found in liver,
 CC fetal liver, bone marrow, placenta, spleen and in lower levels in
 CC skeletal muscle, fetal brain, stomach, lung, thymus, prostate,
 CC brain, mammary, adrenal gland, colon, trachea, cerebellum, testis,
 CC small intestine and spinal cord.
 CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the
 CC termination of the immune response.
 CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. SIGLEC
 CC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AP135027; AAD26428.2; -
 DR EMBL: AF247180; AAF87223.1; -
 DR EMBL: AF227924; AAF71455.1; -
 DR EMBL: AB026265; BAB41100.1; -
 DR EMBL: AC011473; AAG23261.1; -
 DR Genew: HGNC:10878; SIGLEC9.
 DR MTM: 605640; -
 DR GO: GO:0005887; C:integral to plasma membrane; NAS.
 DR GO: GO:0005530; F:lectin; NAS.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00409; Ig; 2.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR Cell adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1
 FT 17
 FT POTENTIAL.

FT	CHAMN	18	463		STATIC ACID-BINDING IG-LIKE LECTIN 9.
FT	DOMAIN	18	348		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	349	369		POTENTIAL.
FT	DOMAIN	370	463		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	20	140		IG-LIKE V-TYPE.
FT	DOMAIN	146	229		IG-LIKE C2-TYPE 1.
FT	DOMAIN	236	336		IG-LIKE C2-TYPE 2.
FT	SITE	431	436		ITIM MOTIF.
FT	SITE	454	459		SLAM-LIKE MOTIF.
FT	DISULFD	36	170		BY SIMILARITY.
FT	DISULFD	41	102		BY SIMILARITY.
FT	DISULFD	164	213		BY SIMILARITY.
FT	DISULFD	272	320		BY SIMILARITY.
FT	CARBOHYD	101	101		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	138	138		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	161	161		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	225	225		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	231	231		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	238	238		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	256	256		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	334	334		N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	VARIANT	100	100		K -> E (1n dbsnp:2075803j).
FT	VARIANT				/FtId-VAR_014254.
FT	VARIANT	125	125		S -> N (1n dbsnp:300658).
FT	VARIANT				/FtId-VAR_014255.
FT	VARIANT	147	147		N -> K (1n dbsnp:273687).
FT	VARIANT				/FtId-VAR_014256.
FT	VARIANT	315	315		A -> E (1n dbsnp:2256983j).
FT	VARIANT				/FtId-VAR_014257.
FT	VARIANT	316	316		A -> D (1n dbsnp:273688).
FT	VARIANT				/FtId-VAR_014258.
FT	MUTAGEN	120	120		R->I: LOSS OF STATIC ACID BINDING.
FT	CONFLICT	269	269		R -> H (1n REF.2)
SO	SEQUENCE	463 AA;	50081 MW;		807BDCED018191F2 CRC64;

```

Query Match      32.2% Score 870: DB 1: Length 463;
Best Local Similarity 39.4% Pred. No. 6.7e-54;
Matches 203: Conservative 77; Mismatches 169; Indels 66; Gaps 12.

OY 5 LLLSLLLGGSGAMDRF--WIRQESVVRPEGLCSIVCSFSYPRDWTGSTP-AUYGF 61
   ||| ||| : : : : : ||| ||| ||| ||| ||| ||| |||
Db 3 LLLRLPLGRRERAGQTSKLLTQSSVVGQSLCNVHCSPSSYPSHGWIYRQVHNGWF 62
OY 62 KAVLETKGAVLANNHOSREVENMTRGFOULTGRPAKNCSLYTRDAQMODESQYFFVE 121
   : : : ||| ||| : : : ||| ||| ||| ||| ||| ||| |||
Db 63 REGANTDDAAVALANNPRAVAWEETRDQFHLIGDRHNKNTLSINDARSDAGREFRME 122
OY 122 RGSYVVRNFMNDGEFFLKYATLTQKRDVYIPETLERGQVUYICVFNMAFEEDSPFSMT 181
   ||| : : : : : ||| ||| : : : ||| ||| ||| ||| |||
Db 123 KGS-IKNNYKHNRLSVNVTALTGNRNLIPETLSEGCQNLTCSPVAKSCDQTPMIMSI 181
OY 182 GAALSQGTKEFTSHFSVLTSPRRQDHTDLTCHVDSRKGVSAQTRVRLVAYARPD 241
   ||| : : : ||| : ||| ||| ||| ||| ||| ||| |||
Db 182 GTSYSP--LDPSTRRSYLTLPDRQDHTSLTQVFERGASVYTNKTVHLNVSY----- 234
OY 242 VISISRDTPRPENRLRYVMSQARTYLENGNSLYLVLAGOSLCLVC---VHTSPRA 298
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| |||
Db 235 -----PRQNLMTVYQGGGTYSTVLGNSSLSLPEQSLRLCAVDAVANDSNRA 283
OY 299 RLSTWTKRQVLSPSQSDPQVLELPRVOVEHEGEFTCHARRPLGSOHSLSYVHKGGL 358
   ||| : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 RLSTSMRGILTCPSQSPNPGVLELRPMVILRADEETCRAQNPDLGQVYLVLSQSK--- 340
OY 359 ISTAFNSGAFGLGIIITALLFLCALILIMKILPKRRTQETETRRPRSRKSTILDIYNY-- 416
   : : : : : ||| ||| : : : ||| ||| ||| ||| ||| |||
Db 341 ATSCVTVGVGGAATLALVELFSCVIFVY---SSCRKKSAPRAGVGDTEIEDNAAVAG 397
OY 417 -PTAGPLAQKRNQKATPNSRPTPLRPGAPSPESKKNOKQYQLPSFPPKSTQAPESQE 475
   ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 SASQGPLTEPMAEDS-----PPQPPRPA$R-----SSV 426
OY 476 SQELNAYATLNFQVRRPRPEAKMKGTDADYAEYK 510
   : || ||| : ||| : : : ||| : : : ||| : : : |||

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Db 427 GEGELQYASLSFQWVPM-DSRGCEADTETSEIK 460

RESULT 8

ID	NAME	STANDARD	PRT	442 AA.
AC	CD33699	015388; 043700;		
AD	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Stallid acid binding Ig-1-like lectin 6 precursor (siglec-6) (obesity-binding protein 1) (OB-BP1) (CD33 antigen-like 1).			
GN	SIGLEC6 OR CD33L OR CD33L1 OR OBSP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Placenta;			
RX	Medline=99357812; Pubmed=9465907;			
RA	Tekel Y., Sasaki S., Fujiwara T., Takahashi E., Mito T., Nakamura Y.;			
RT	"Molecular cloning of a novel gene similar to myeloid antigen CD33 and its specific expression in placenta.";			
RL	Cytogenet. Cell Genet. 78:295-300(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH LEP.			
RC	TISSUE=Erythrocyte/leukemia;			
RX	Medline=99357812; Pubmed=10428850;			
RA	Patel N., Brinkman-Van der Linden E.C.M., Altman S.W., Gish K.C.,			
RA	Balasubramanian S., Tlams J.C., Peterson D., Bell M.P., Bazan J.F.,			
RA	Varki A., Kastelein R.A.;			
RL	J. Biol. Chem. 274:28058-28058(1999).			
CC	-1- FUNCTION: Putative adhesion molecule that mediates stialic-acid dependent binding to cells. Binds to alpha2,6-linked stialic acid.			
CC	The stialic acid recognition site may be masked by cis interactions with stialic acids on the same cell surface.			
CC	-1- SUBUNIT: Interacts with LEP.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1: Synonyms=Membrane-bound, CD33L1;			
CC	Isoid=043699-1: Sequence=Displayed;			
CC	Name=2: Synonyms=Secreted, CD33L2;			
CC	Isoid=043699-2: Sequence=VSP_002553, VSP_002554;			
CC	Note=Should not be confused with SIGLEC5 which has been called CD33L2;			
CC	-1- TISSUE SPECIFICITY: Expressed at high levels in placenta (cyto- and syncytiotrophoblastic cells) and at lower levels in spleen, peripheral blood leukocytes (predominantly B-cells) and small intestine.			
CC	-1- DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (STIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.			
CC	-----			
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RN [5]
 RP FUNCTION.
 RX MEDLINE=20079612; PubMed=10611343; Ponte M., Vitale M., Moretta A.,
 RA Vitale C., Romagnani C., Falco M.,
 RA Baccigalupo A., Moretta L., Mingari M.C.;
 RT 'Engagement of p75/FAIR1 or CD33 inhibits the proliferation of normal
 RT or leukemic myeloid cells';
 RL Proc. Natl. Acad. Sci. U.S.A. 96:15091-15096(1999).
 RL [6]
 RP DISIALOGLANGLOSIDE BINDING.
 RX MEDLINE=21286126; PubMed=11389909;
 RA Ito A., Handa K., Withers D.A., Satoh M., Hakomori S.;
 RT 'Binding specificity of siglec7 to disialogangliosides of renal cell
 RT carcinoma: possible role of disialogangliosides in tumor
 RT progression';
 RL FEBS Lett. 498:116-120(2001).
 CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3 and
 CC alpha2,6-linked sialic acid. Also binds disialogangliosides
 CC (disialoagangliosyl globoside, disialyl lactotetraosylceramide and
 CC disialyl GalNAc lactotetraosylceramide). The sialic acid
 CC recognition site may be masked by cis interactions with sialic
 CC acids on the same cell surface. In the immune response, may act as
 CC an inhibitory receptor upon ligand induced tyrosine
 CC phosphorylation by recruiting cytoplasmic phosphatase(s) via their
 CC SH2 domain(s) that block signal transduction through
 CC dephosphorylation of signaling molecules. Mediates inhibition of
 CC natural killer cells cytotoxicity. May play a role in hemopoiesis.
 CC Inhibits differentiation of CD34+ cell precursors towards
 CC myelomonocytic cell lineage and proliferation of leukemic myeloid
 CC cells (in vitro).
 CC -1- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=4;
 CC Name=1; Synonyms=AIKM-1b;
 CC IsoId=Q9Y286-1; Sequence=Displayed;
 CC Name=2; Synonyms=AIKM-2;
 CC IsoId=Q9Y286-2; Sequence=VSP_002555;
 CC Name=3; Synonyms=AIKM-3;
 CC IsoId=Q9Y286-3; Sequence=VSP_002556, VSP_002558;
 CC Note=No experimental confirmation available;
 CC Name=4;
 CC IsoId=Q9Y286-4; Sequence=VSP_002557, VSP_002558;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Predominantly expressed by resting and
 CC activated natural killer cells and at lower levels by granulocytes
 CC and monocytes. High expression found in placenta, liver, lung,
 CC spleen, and peripheral blood leukocytes.
 CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the
 CC termination of the immune response. The phosphorylated ITIM motif
 CC binds to the SH2 domain of PTPN6/SHP-1.
 CC -1- PTM: Tyrosine-phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
 CC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 406.
 CC -----
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 CC -----
 DR EMBL; AF170485; AAF12759.1; -;
 DR EMBL; AJ0007395; CAB46011.1; -;
 DR EMBL; AJ130710; CAB51126.1; -;

DR	EMBL:	AJ130711;	CAB51127.1;	-
DR	EMBL:	AJ130712;	CAB51128.1;	-
DR	EMBL:	AJ130713;	CAB51129.1;	-
DR	EMBL:	AF178981;	AAF4436.1;	ALT_FRAME.
DR	EMBL:	AF193441;	AAFO6790.1;	-
DR	Genev:	HGNC:10876;	SIGLEC7.	
DR	MIM:	604410;	-	
DR	GO:	GO:0005987;	C:integral to plasma membrane; TAS.	
DR	GO:	GO:0005530;	F:lectin; TAS.	
DR	GO:	GO:004872;	F:receptor activity; TAS.	
DR	InterPro:	IPR007110;	Ig-like.	
DR	InterPro:	IPR003598;	Ig-C2.	
DR	InterPro:	IPR003006;	Ig-MHC.	
DR	Pfam:	PF00047;	Ig_3	
DR	SMART:	SM00408;	IGc2; 1.	
DR	PROSITE:	PS50835;	IG-LIKE; 2.	
KW	Cell adhesion;	Lectin; Transmembrane; Signal; Glycoprotein;		
KW	Immunoglobulin domain;	Repeat; Phosphorylation; Alternative splicing.		
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	467	STATIC ACID BINDING IG-LIKE LECTIN 7.
FT	DOMAIN	19	353	EXTRACELLULAR (POTENTIAL).
FT	TRANSMM	354	376	POTENTIAL.
FT	DOMAIN	377	467	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	39	122	IG-LIKE V-TYPE.
FT	DOMAIN	150	233	IG-LIKE C2-TYPE 1.
FT	DOMAIN	240	336	IG-LIKE C2-TYPE 2.
FT	SITE	435	440	ITIM MOTIF.
FT	DISELFD	46	106	BY SIMILARITY.
FT	DISELFD	168	217	BY SIMILARITY.
FT	DISELFD	276	320	BY SIMILARITY.
FT	CARBOHD	105	105	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	142	142	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	165	165	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	229	229	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	235	235	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	242	242	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	260	260	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHD	334	334	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	VARSPLIC	145	238	ALTRPNLPILPGTLESGCFOMLTCSVPMAECGPRLMSM GTSPSLPHTSRSSVTLPIPODHNHSTSLTCOVTLPCAGV TNRTIOLNVS -> D (In isoform 2).
FT	VARSPLIC			/FtId-VSP_002555.
FT	VARSPLIC	145	145	A -> E (In isoform 3).
FT	VARSPLIC	145	145	/FtId-VSP_002556.
FT	VARSPLIC	146	467	A -> G (In isoform 4).
FT	VARSPLIC			/FtId-VSP_002557.
FT	CONFLICT	42	42	Missing (In isoform 3 and isoform 4).
FT	SEQUENCE	467 AA;	51142 MM;	/FtId-VSP_002558. V -> A (In REF. 4). BAPE44462B00LF52 CRC64;
SO	Query Match			
	Best Local Similarity	30.8%;	Score 832.5;	DB 1; Length 467;
	Matches	198;	Conservative	78; Mismatches 174; Indels 73; Gaps 11.
OY	2	LLPLLSSLDCGSQAMGR-----FWRVDSVWPVRGCLGISVPCSFSTRPDWTGSTR	55	
Db	1	MLLLLLPLLMGRREVGECKSNRRDYSLTMOSSVYVGCMCVHNCSPSYSDTSDDP	60	
OY	56	AYGWFKAVTEETGAPVATNHQSREVNSTRGFOLGDPKAKGCSVIRDAQMDSEQ	115	
Db	61	VHGIVFRAGNDISMKAPATNNPPAAYOEFTRDRRHLLGDGYTKRKCTISIDARRSADGR	120	
OY	116	YFFRVERGSYVRNFPMNDFFLKVTALTKQRPDUYIPETLRGQPVTVICVENNAFECP	175	
Db	121	YFFRMERKEN-IKMWKYKLDQLSVNVATLHRNPRIILPTGLESGCFONLTCSVPMACEOGTP	179	
OY	176	PSFWMGTAALSQGKPTTSHFSVFSTRPDODDTDLTGVDVDSRKGVSAQRVRYRLVA	235	
Db	180	PMISMGTGVSPP--LHPSTRSSVYLTIPIPODHNHSTSLTCOVTLPGAGVTTNRITQLNVS	237	
OY	236	YAPRDLYVISRDNTPPDPENLRVWVSQAQNTVLENLGNGTSLPLEGOSGLICVTHSS	295	

SQ SEQUENCE 551 AA; 60715 MW; 2FEA2B6B341EFAF CRC64;
 Query Match 29.7%; Score 804.5; DB 1; Length 551;
 Best Local Similarity 33.8%; Pred. No. 3.3e-49;
 Matches 206; Conservative 70; Mismatches 172; Indels 161; Gaps 11;

OY 2 LPLPLLSLL-GGSOAMDGRFMIKRVQESVWVWPEGLCISVPCSFSPYPRODGTSTPAYGYW 60
 Db 1 MLPLLLPLLMGSLGDEKPYELQVQKSVYVQGLCVLVPCSFSPYRMSVSSPLLYVW 60
 OY 61 FAVVTTTGAPATVTHQSEVEMSTRGRQLTGDPKAGCSLVYDAQMODSOFYFRV 120
 Db 61 FRCGEIPVYAEVATNNPRKVRPEQGRFLLGDVQKKCSISIGARMEDGYSYFFRV 120
 OY 121 ERGSYRVNPMNDGFLKVTALQKPDVYPTLEPGOPVTVCVFNMAEECPPEFSM 180
 Db 121 ERGRDVKYSYQCKKLEVTALAEKPDHLEPLESGRPRFRLCSLPSCSEADPPPLTFSM 180
 OY 181 TGAALSSOGTKPTTSHFSVLSFTPRQDHDLTCHVDSRKVSQRTVRLVAYAPRD 240
 Db 181 TGNALSP--LDPETTRSSSELTLPREDHGTNLTCQMKRQAGVTTERTVQLNVSAPQT 238
 OY 241 LVYSISRDNTPPDPENLRWVNSQANTVLENLNGNLSLPVLEQSLCLVCTVTSPPARL 300
 Db 239 ITTF-----RNGIALEILLONTSTYLPVLEGOALRLCLDAPSNPAPHL 279
 OY 301 SPTQRGVLPSPQSDPGLVLEPRVOVHEGEFTCAHAPHLGSOHSLSLVHKGLIS 360
 Db 280 SNEGSPALNATPISMTGILELRVRSABEGGTCNAQHPGLQIFLNLSVSLPQLLG 339
 OY 361 TAFS----- 364
 Db 340 PSCSWAEGLHCRCSEFARAPAPSLCWRLEKPLEGNSQGSFKVNSSAGPMANSLILH 399
 OY 365 -----NGAFL-----GIGTALLFLCLALIM 386
 Db 400 GGLISLQKVCAMWNIYSGSGSVLLQGRSNLTGVPVPAALGAGMALLCICLCIF 459
 OY 387 KILPKRRTQETPRPRFSRSTILDYINVPYTAGPLAOKRKNKATPNSPTPL-PPGAPS 445
 Db 460 LIYKARRKQA-AGRPEKMDDED-----PIMGITSSGRKKPWPDSPPDOASPPEDAP 510
 OY 446 PESKKKQKKOYOLPSFPEPKSSQADSESOEELHYATLNFPPRRPRAPRKPTQA- 504
 Db 511 P-----LEEKELHYASLSFSEMK-----SREPKQDEAP 539
 OY 505 ----DYAEVK 510
 Db 540 STTEYSEIK 548

RESULT 11
 CD33_HUMAN STANDARD: PRT; 364 AA.
 AC P20138; Q8TD24;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Myeloid cell surface antigen CD33 precursor (gp67) (Siglec-3).
 GN CD33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Promonocytic lymphoma;
 RX MEDLINE=89009814; PubMed=3139766;
 RA Simmons D., Seed B.;
 RT "Isolation of a cDNA encoding CD33, a differentiation antigen of
 myeloid progenitor cells.";
 RL J. Immunol. 141:2797-2800(1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21940633; PubMed=11943481;
 RA Yousef G.M., Ordon M.H., Fousias G., Diamandis E.P.;
 RT "Genomic organization of the siglec gene locus on chromosome 19q13.4
 and cloning of two new siglec pseudogenes.";
 RL Gene 286:259-270(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Urdin T.B., Toshilyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SIALIC ACID BINDING.
 RX MEDLINE=95235021; PubMed=7718872;
 RA Freeman S.D., Kelm S., Barber F.K., Crocker P.R.;
 RT "Characterization of CD33 as a new member of the sialoadhesin family
 of cellular interaction molecules.";
 RL Blood 85:2005-2012(1995).
 RN [5]
 RP FUNCTION. PHOSPHORYLATION OF TYR-340 AND TYR-358, MUTAGENESIS OF
 TYR-358, AND INTERACTION WITH PRPN6.
 RX MEDLINE=20025980; PubMed=10556798;
 RA Uyanova T., Blasoli J., Woodford-Thomas T.A., Thomas M.L.;
 RT "The sialoadhesin CD33 is a myeloid-specific inhibitory receptor.";
 RL Eur. J. Immunol. 29:3440-3449(1999).
 RN [6]
 RP PHOSPHORYLATION OF TYR-340 AND TYR-358, INTERACTION WITH PRPN6 AND
 PRPN11, AND MUTAGENESIS OF TYR-340.
 RX MEDLINE=99223460; PubMed=10206955;
 RA Taylor V.C., Buckley C.D., Douglas M., Cody A.J., Simmons D.L.,
 RA Freeman S.D.;
 RT "The myeloid-specific sialic acid-binding receptor, CD33, associates
 with the protein-tyrosine phosphatases, SHP-1 and SHP-2.";
 RL J. Biol. Chem. 274:11505-11512(1999).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=21244678; PubMed=11320212;
 RA Vitale C., Romagnani C., Puccetti A., Olive D., Costello R.,
 RA Chiosso L., Pizzo A., Baccigalupo A., Moretta L., Mingari M.C.;
 RT "Surface expression and function of p75/ATR-1 or CD33 in acute
 myeloid leukemias: engagement of CD33 induces apoptosis of leukemic
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5764-5769(2001).
 CC -I- FUNCTION: Putative adhesion molecule of myelomonocytic-derived
 cells that mediates sialic-acid dependent binding to cells.
 CC Preferentially binds to alpha2,6-linked sialic acid. The sialic
 CC acid recognition site may be masked by cis interactions with
 CC sialic acids on the same cell surface. In the immune response, may
 CC act as an inhibitory receptor upon ligand induced tyrosine
 CC phosphorylation by recruiting cytoplasmic phosphatase(s) via their
 CC SH2 domain(s) that block signal transduction through
 CC dephosphorylation of signaling molecules. Induces apoptosis in
 CC acute myeloid leukemia (in vitro).
 CC -I- SUBUNIT: Interacts with PRPN6/SHP-1 and PRPN11/SHP-2 upon

phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Monocytic/myeloid lineage cells.
 CC -1- DOMAIN: Contains two copies of an intracytoplasmic motif referred
 CC as immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 CC motif is involved in downmodulation of cellular functions as the
 CC termination of the immune response. The phosphorylated ITIM motif
 CC binds to the SH2 domain of PTPN6/SHP-1 and/or PTPN11/SHP-2.
 CC -1- PHOSPHORYLATION: Phosphorylated on tyrosine residues.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SILEC
 CC (SILEC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- DATABASE: NAME-PROV; NOME-CD guide CD33 entry;
 CC WWW-<http://www.ncbi.nlm.nih.gov/prov/cd/cd33.htm>.
 CC
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 CC
 DR EMBL: M23197; AAA51948.1; ALT_SEQ.
 DR EMBL: AY040541; AAH83654.1; -;
 DR EMBL: BC028152; AAH28152.1; -;
 DR PIR: A30521; A30521.
 DR HSSP: Q62230; IQFO.
 DR Genev: HGNC:1659; CD33.
 DR MIM: 159590; -;
 DR GO: GO:0005872; C: integral to plasma membrane; TAS.
 DR GO: GO:0004872; F: receptor activity; TAS.
 DR GO: GO:0007267; P: cell-cell signaling; TAS.
 DR GO: GO:0008285; P: negative regulation of cell proliferation; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; Ig; 2.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Cell adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein;
 KW Phosphorylation; Immunoglobulin domain; Repeat; Multigene family;
 FT SIGNAL 1 17
 FT CHAIN 18 364
 FT DOMAIN 18 259
 FT TRANSMEM 260 282
 FT DOMAIN 283 364
 FT DOMAIN 19 135
 FT DOMAIN 145 228
 FT SITE 338 343
 FT SITE 356 361
 FT DISULFID 36 169
 FT DISULFID 41 101
 FT MOD_RES 163 212
 FT MOD_RES 340 340
 FT MOD_RES 358 358
 FT CARBOHYD 100 100
 FT CARBOHYD 113 113
 FT CARBOHYD 160 160
 FT CARBOHYD 209 209
 FT CARBOHYD 230 230
 FT MUTAGEN 340 340
 FT MUTAGEN 358 358
 FT CONFLICT 69 69
 FT SEQUENCE 364 AA; 39726 MW; 1973E196940FB16F CRC64;
 Query Match 25.68; Score 694; DB 1; Length 364;

Best Local Similarity 32.8%; Pred. No. 1,1e-41;
 Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;
 QY 1 MLPLLSLLGSGQAMDRFMIRVOESWVBEGLCTVPCSFSTPRDWTGSTAYGW 60
 Db 1 MFLPLPLPLMGALAMDENFWLQVSETVBEGGLVPCFEPFIPYDKNSPVHGWM 60
 QY 61 FAVETTTGAVATVTHOSREVENSTGRFQLTGPANGKSLVTRDQOMDESOYFRV 120
 Db 61 FREGALISDSDPVATNKIDQVEYEGFRLGDPSSKNSLSIVDARRRNGSYFFRM 120
 QY 121 EGGSVYRVFEMDGFLLKVTALTQKPDVYIPETLEPGQPVTVCFVMAFECPSPFSW 180
 Db 121 EGGV--TKSYSKSPQSLSVHTDLTHRPKILIPETLEPGHSHKSLTCSVMAEQGPPIPSW 179
 QY 181 TGAALSSQGTPTTSHFVSFTPPRODHDLCHVDYFSGKYSAGRTVLRVAYARD 240
 Db 180 LSAAPTSLG--PRTHSSVLTTPRQDHGTLNLCQVFAAGVTTERTIOLANTVYVON 237
 QY 241 LVISISRDNTDPPENLRVWVSOANRVLNENIGNSTSLPVEGSLICLVTHSSPARL 300
 Db 238 PTTGTFP-----GDG----- 247
 QY 301 SMTQGVLSPSQSPDQVLELPRVQVEHEGEFTCHARHPLGSOHVSLSVHYKGLIS 360
 Db 248 -----SGKQETRAGV----- 258
 QY 361 TAFNSGAFVIGITATFLCLALINILPKRRQTQTEPRPFRSHSTIIDYINVPAG 420
 Db 259 ---HGAIGAGVATALLALCLCLFLFTVKTTHRAARTAVGRNDTH-----PTTG 304
 QY 421 PLAKRQKATPPNSPRIPPLPGAPSPESKQKQYOLPSPFEPKSTQAPESQSEQL 480
 Db 305 SASRHKQKSLHGP-----TETSSCSGAAPVEMDEEL 338
 QY 481 HYATLFPVYPRPEARMKPGTQADVAEVKQ 512
 Db 339 HYASLNFHGMN-----SKDITREYSEVARTQ 364
 RESULT 12
 SILE_MOUSE STANDARD; PRT; 569 AA.
 ID SILE_MOUSE
 AC Q920G3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Stailic acid binding Ig-like lectin-F precursor (mSiglec-F).
 GN SiglecF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=21576254; PubMed=11579105;
 RA Angata T., Hingorani R., Varki N.M., Varki A.;
 RT Cloning and characterization of a novel mouse Siglec-F;
 RT differential evolution of the mouse and human (CD33) Siglec-3-related
 RT gene clusters.;
 RL J. Biol. Chem. 276:45128-45136(2001).
 CC -1- FUNCTION: Putative adhesion molecule that mediates stailic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3-
 CC linked stailic acid. The stailic acid recognition site may be masked
 CC by cis interactions with stailic acids on the same cell surface.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed by immature
 CC monocytic/myeloid lineage cells in bone marrow. Also found at
 CC lower levels in mature neutrophils and monocytes.
 CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the

```

CC      termination of the immune response.
CC      -1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC      (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AF293371; AAL11043.1; -.
CC      InterPro: IPR007110; Ig_L1ke.
CC      InterPro: IPR003598; Ig_C2.
CC      InterPro: IPR003006; Ig_MHC.
CC      Pfam: PF00047; Ig_2.
CC      SMART: SM00408; IgC2; 1.
CC      PROSITE: PS50835; IG_Like; 2.
CC      Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
CC      Immunoglobulin domain; Repeat.
CC      KW      SIGNAL 1 16 POTENTIAL.
CC      FT      CHAIN 1 16 POTENTIAL.
CC      FT      DOMAIN 17 569 SIALIC ACID BINDING IG-LIKE LECTIN-F.
CC      FT      TRANSMEM 17 439 EXTRACELLULAR (POTENTIAL).
CC      FT      DOMAIN 440 460 POTENTIAL.
CC      FT      DOMAIN 461 569 CYTOPLASMIC (POTENTIAL).
CC      FT      DOMAIN 18 116 IG-LIKE V-TYPE.
CC      FT      DOMAIN 139 224 IG-LIKE C2-TYPE 1.
CC      FT      DOMAIN 229 324 IG-LIKE C2-TYPE 2.
CC      FT      SITE 336 541 ITIM MOTIF.
CC      FT      SITE 559 564 SLAM-LIKE MOTIF.
CC      FT      DISULFID 35 163 BY SIMILARITY.
CC      FT      DISULFID 40 96 BY SIMILARITY.
CC      FT      DISULFID 157 206 BY SIMILARITY.
CC      FT      DISULFID 265 308 BY SIMILARITY.
CC      FT      CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT      CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      SQ      SEQUENCE 569 AA; 61476 MW; 8093838090484FC1 CRC64;

Query Match      25.5%; Score 689.5; DB 1; Length 569;
Best Local Similarity 30.8%; Pred. No. 4,1e-41;
Matches 191; Conservative 79; Mismatches 178; Indels 173; Gaps 18;

OY      2 LRLPLLSLLGSGAAMDGRFWIRVYQESVWVPEGLCISVPCSFSPRQDMTGSTPAYGYWF 61
DB      6 LRLPLMA-----GCLALDGS-YSLSYVSGSVYVQEGLCVFVACQVYF-----NSKGPVVGWYF 56
OY      62 KAVETTTKGA PVATNHSREVEKSTRGFOQTGDPKAGKNCSLVIRDAQMDQESQYEFVFE 121
DB      57 REGANIFSGSPVATNDPORSVLKEAGREVLKMGKNSHNCSLDIRDAOKIDTGYTFEFLD 116
OY      122 RGSVYRNFMNMGDFLAKVATLQKQPDVYIPETLEPQOPVYICVFWMAREDECPSPFSWT 181
DB      117 -GS-VKYSFOKSMLSLVLTALTEVPNIQVTSLVSGNSKLLCSVMACEQGPPIFSWM 174
OY      182 GAALSQGTQKPTTSHFSVLSFTPRPDHDTDLCHVDFSRKGVSAQRTVLRVAVAPRDL 241
DB      175 SSALTSLSGHTTSL--SELNITPRPDNTNLTQVNLPGTGVTVERTQOLSTIYA-----228
OY      242 VISISDNTPDPPENLRVMSQANRTVLENLNGTSLPYLVEGSGTCLVLCVTHSSPPARLS 301
DB      229 -----POKMTIRVSWGDDTGTFVQLSGASLTQIOEGSLSLVCVMAADSNPVALVS 276
OY      302 KTRGQGVLSPSQPSDGVLELPRVQVEHGEFTHARHRLPGSGHVSLSLV-----352
DB      277 WERPTQ--KPFQSTLPAELQLPRAELEDQGYTCQANQSGAQTASVLSLSIRSLQLLGP 334

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OY      353 -----HYRKG-----LISF 361
DB      335 SCSEFEGGLHCSSSNRAMPAPSLRWIRGEEVLGNSNSGFTWKSSSAGQMANSSILSM 394
OY      362 AFSN-----GAFIGITALLFLC 380
DB      395 EFSNHRSLSCAENDNRVQATILVSGPKVSOAGKSETSRGTVLCAIMWAGLALLAVC 454
OY      381 LALIT--MKLPRRRQTEPRRFRSHSTILDIYINVPVAGLAKRKNKATPNSPRTP 438
DB      455 LCILFTVYKVLRRKSA-----LVAAKRGHHLAK-NPASTINS----491
OY      439 LPPGAPSESKKQKQYOLPS-FPEPKSSTQ-----APSSQSEELHYATILNFPG 489
DB      492 -----ASTSSNIALGTYPIQGLNBERGSGTQKQEPPLAVPDTQKDEPRLHYSLSFQ 545
OY      490 VRPRPARMPKGTQADYAEVK 510
DB      546 PMP-PRPQNTKAMKSVYTEIK 565

RESULT 13
CD33_MOUSE
ID      CD33_MOUSE STANDARD; PRT; 403 AA.
AC      063994; 063997;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Myeloid cell surface antigen CD33 precursor (Siglec-3).
GN      CD33.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 33-A AND 33-B).
RX      STRAIN-BALB/C; TISSUE-Bone marrow;
RX      MEDLINE=94250900; PubMed=8193354;
RA      Tchilian E.Z., Beverley P.C., Young B.D., Watt S.M.;
RT      Molecular cloning of two isoforms of the murine homolog of the
RL      myeloid CD33 antigen.
RL      Blood 83:3188-3198(1994).
CC      -1- FUNCTION: Putative adhesion molecule of myelomonocytic-derived
CC      cells that mediates stialic-acid dependent binding to cells.
CC      Preferentially binds to alpha2,6-linked stialic acid (by
CC      similarity). The stialic acid recognition site may be masked by cis
CC      interactions with stialic acids on the same cell surface.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Name=33-B;
CC      IsoId=Q63994-1; Sequence=Displayed;
CC      Name=33-A;
CC      IsoId=Q63994-2; Sequence=VSP_002534;
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
CC      (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: S71345; AAB30842.1; -.
CC      EMBL: S71403; AAB30843.2; -.
CC      MGD: MGI:99440; CD33.
CC      InterPro: IPR007110; Ig_L1ke.
CC      InterPro: IPR003599; Ig.

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Query Match		11.28;	Score 303.5;	DB 1;	Length 626;
Best Local Similarity		21.18;	Pred. No. 57e-14;		
Matches 137;	Conservative	90;	Mismatches 229;	Indels 193;	Gaps 23;

21 FWIWO-----ESWMEVGLGICISPPCSFSPYPRDWMGSSPDPAYGVWFKAIVFTT 6R

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DB      10 FMIMISASRGHGMAMPSSISAIFEGTCSIPCRDFP--DELRAVAVGVYFNSPYPK 67
        69 KCAPATNQHSEVEMSTRGRFQLTGDPAKNCSLVINDAQODESQVFRERERSYAK 128
        68 NYPPEVKSRIQVHESFQGRSRLGLDGLRNCRTLLLSVSPSELGKYYFRIDLCGYNOY 127
        129 NFMNDGFLKVTALQKPDVYIPETLEPQOPVTVCVFMMAFEECP--PSSMTG---- 182
        128 TFSEH----SVLDIYNTNINIVYPRVAVGTEVEVSCMP--DNCEPRLPELSWIGHHEL 180
        183 ---AALSS-QGTRKPTTSHFSVLSFTPRQDHDITLCHVDSFRKCVSAQRTVRLRAYAP 238
        181 GEPALVGLRDEDEGTAVQVSLHFPVTRRANGRLGCAQSPFNTLLQFEGYASMDYKXP 240
        239 RDLVISIS-----RDNTPPD-----PENLRVMY----- 261
        241 VIVEMNSSVEALEGSHVSLLCGADSNPPPLLTMMRDGTVLREAVAESLLELEEVTPAED 300
        262 -----SQARNTV-----LENLNGTSLPYLEGGSLCIVCTHSSPPARLSM 302
        301 GYVACLAEVAGQDKRTVGLSVYAPKPTVNGTVAVY-EGETVSLTCTQSNPDPILTI 359
        303 TORGVLSPPSPDGVLELPRVQVEHEGEFTCHARHPLGSGHVSLSLVHYKKGIL--- 359
        360 FKEKQILSTVIESELELPAVSPEDDEGEYVCVAENQGRATAFNLISVEFAPVLLLES 419
        360 -----STAF-----SNGAFL-----GIGTALLFLCIA 382
        420 HCAARDVVOCLCVVKSNDPEVAPELPSRNTVNESEREFEVYSRSGLVLSITLTL--- 476
        383 LIIMILPKRRTQTEP-----RPRSRHSTILDY-----INVPTAGPLA---- 423
        477 -----KQQAAPPRVITATANLGLAKSLERFQCAHMLMAKIPVCAVAVFAIL 526
        424 -----OKRQKATPNSPRTPLP-----GAPSP-ESKKKQKQYQLPSF 461
        527 IAIVCYITQTRKKKNTVESPSACDNPPVLFSSDFRISGADEKESERLSERLTGL 586
        462 PEPKSTQAPESQSEELHYATLNFPCVPRPPEARMRGTOADAEVK 510
        567 -----KGEPELLDLSYSHDL-GKRPKDSYTLTEELAEYAEIR 624

RESULT 15
SMP_COTJA STANDARD: PRT: 620 AA.
ID SMP_COTJA          STRAND:          PRT:          620 AA.
AC 092154;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Schwann cell myelin protein precursor (Siglec-4b).
GN CN
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
OX
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-28; 120-132; 135-157 AND
RP 563-571.
RX MEDLINE=92153423; PubMed=1739462;
RA Dulac C., Tropak M.B., Cameron-Curry P., Rossier J., Marshak D.R.,
RA Roder J., le Douarin N.M.;
RT "Molecular characterization of the Schwann cell myelin protein, SMP;
RT structural similarities within the Immunoglobulin superfamily.";
RL Neuron 8:333-334(1992).
CC -1- SUPRACELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Exclusively expressed by myelinating and
CC nonmyelinating schwann cells and oligodendrocytes.
CC -1- DEVELOPMENTAL STAGE: First synthesized at embryonic day 5, 1t
CC remains expressed by cultured Schwann cells.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC

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CC      (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL: S83711; AAB21466.1; -.
CC      PIR: JH0593; JH0593.
CC      HSP: P56276; ITLK.
CC      InterPro: IPR007110; Ig-like.
CC      InterPro: IPR003598; Ig_C2.
CC      InterPro: IPR003006; Ig_MHC.
CC      SMART: PF00047; Ig_2.
CC      SMART: SM00408; IgC2_2.
CC      PROSITE: PSS0835; IG_LIKE_2.
CC      Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
CC      Immunoglobulin domain; Repeat.
CC      CHAIN 1
CC      DOMAIN 18 620
CC      DOMAIN 18 516
CC      TRANSMEM 517
CC      DOMAIN 537 620
CC      DOMAIN 28 106
CC      DOMAIN 151 233
CC      DOMAIN 325 407
CC      DOMAIN 414 485
CC      DOMAIN 35 164
CC      DISULFID 40 99
CC      DISULFID 158 216
CC      DISULFID 260 304
CC      DISULFID 346 391
CC      DISULFID 420 429
CC      DISULFID 431 488
CC      CARBOHYD 222 222
CC      CARBOHYD 314 314
CC      CARBOHYD 331 331
CC      CARBOHYD 405 405
CC      CARBOHYD 449 449
CC      SEQUENCE 620 AA; 66943 MW; 004B3EC7EBC18FBA CRC64;

Query Match 11.2%; Score 302.5; DB 1; Length 620;
Best Local Similarity 22.4%; Pred. No. 6, 6e-14;
Matches 148; Conservative 89; Mismatches 224; Indels 199; Gaps 29;

OY      5 LLLSLIGSQAMDGRFMIRVOESVAVPBGCLISVYCSFSYRQDMTGSTPAY--GYWPK 62
        4 LVLTVLIMGTGCSISAPWAMMPKMAALSGTCVOQLCRPDYEE---LRPASIGLWY- 58
        63 AVTEETKCAP-----VATNQHSEVEMSTRGRFQLTGDPAKNCSLVINDAQODE- 113
        59 -----FGSPYKNTNPPVYARSPSSAVIHESFAGRASFLGDPTRGRTLINI--ARLSEEL 110
        114 -SOYFFRVERGSAVRYNFMNDGEFLKVTALQKPDVYIPETLEPQOPVTVCVFMMAFEE 172
        111 ACKYFERGDLGYNQSF--SEHAELDYMA---APHLEVHELIVAGSEAEILCRV--DN 163
        173 CPP--PSEFWTGA--ALSSQGR-----PTTSHFSVLSFTPRQDHDITLCHVDSFRK 222
        164 CPEPLRLMLTTEELDPIGKERLEDLGSLSGLSLFRPKKEDLGRVVGCVFIINS 223
        223 GVSAGRTVRLRAYAPR-----DLVISISRDNTP-----DP 253
        224 SISFQADVGLDYOYERQVVGGLGPTVYVGSDELCEABGRAPLISFRGSEVAREEP 283
        254 PENLRVMSQAN-----RTYLEN-----LGNGTSLPYLEGGSL 286

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Db      284 GRNRLLLSNVGPDDGGSFSCVAENNRHNRSLQLRAVAPARAPYING-SLMVYSGDPV 342
QY      287 CLVCYTHSSPPARLSMTORGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHPLGSGHV 346
      : | | | | : | | : | | : | | : | | : | | : | | : | |
Db      343 SVTCRAESEEPAILVLRGCKYMAAAIYDHYTMEKRRPARPEDGTTSCVAENOHGASST 402
QY      347 SLSLSVHYKKGLI-----STAF----- 363
      | : | | | : |
Db      403 SFNISVEYPPPLVLPASRCTAGSDGVRCVMVNSIPDSSLVFELPTRNQTVSDGHRDFTAA 462
QY      364 ---SNGAFILGIGIT-----ALLFLCLALLIMKILPKRKRYOTETPRPRFSRH----- 406
      | : | | | | : | | | | : | | : | | : | |
Db      463 PPGSDGSITGL-LTLRGLPEPRLVLCAA-----RNRHGTAROLRFHHPGGIWMAK 513
QY      407 ---STILDYINVPPTAGPLAQKRNQKATPNSPRTPLPP-----GAPSPESKKNQ----- 452
      : : | | : | | : | | : | | : | | : | | : | |
Db      514 VGPVCAVVAFAIVAVVCLSGSRKKAGSPETPVQPMAGPGGDDPLDLRPOQVYRWLR 573
QY      453 ---KKQYQLPSFPPEPKSSTQAPESQSQEELHYATLNFPGVRRPRPEARMKGTQADYAEVK 510
      : : | | : | | : | | : | | : | | : | | : | |
Db      574 GAMERWAL-----GVKEGSGGAP--QEVTPTSH-----PPMKP--TRGPLEDDPEYAEIR 618
```

Search completed: October 8, 2003, 20:03:37
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2003, 17:25:21 : Search time 64 Seconds
(without alignments)
2064.421 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLSLIGSQAMDGR.....RPEARMPKCTQADYAEVKRQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1211.5	44.8	623	11	QB8Y18	QB8Y18 mus musculu
2	909	33.6	568	4	QB1YH7	QB1YH7 homo sapien
3	664	24.5	269	11	QB8T62	QB8T62 mus musculu
4	530.5	19.6	304	4	QB1W38	QB1W38 homo sapien
5	471.5	17.4	423	11	QB8U57	QB8U57 mus musculu
6	371.5	13.7	287	4	QB9P08	QB9P08 mus musculu
7	360.5	13.3	269	6	QB9KP9	QB9KP9 homo sapien
8	358.5	13.2	271	6	QB9KQ0	QB9KQ0 gorilla gor
9	351.5	13.0	269	6	QB9SKP8	QB9SKP8 pan paniscu
10	235.5	8.7	312	6	QB95JN1	QB95JN1 pongo pygma
11	205	7.6	430	4	QB15600	QB15601 macaca fasc
12	198.5	7.3	367	11	QB9P4M0	QB9P4M0 homo sapien
13	195.5	7.2	461	4	QB13854	QB13854 mus musculu
14	194.5	7.2	461	4	QB0430	QB0430 homo sapien
15	186.5	6.9	508	11	QB8R007	QB8R007 mus musculu
16	186.5	6.9	508	11	QB8CED8	QB8CED8 mus musculu

17	184	6.8	402	11 Q35444	Q35444 mus musculu
18	183	6.8	483	11 Q9DBP8	Q9DBP8 mus musculu
19	182.5	6.7	577	11 Q9DZ21	Q9DZ21 mus musculu
20	177	6.5	510	4 Q96N78	Q96N78 homo sapien
21	175.5	6.5	1252	11 Q9J1X2	Q9J1X2 rattus norv
22	175	6.5	510	4 Q96K15	Q96K15 homo sapien
23	175	6.5	662	4 Q60926	Q60926 homo sapien
24	167	6.2	464	4 Q16170	Q16170 homo sapien
25	167	6.2	468	4 Q96CA7	Q96CA7 homo sapien
26	166.5	6.2	718	5 Q21139	Q21139 caenorhabdl
27	166.5	6.2	1332	5 Q9BN17	Q9BN17 drosophila
28	166.5	6.2	1332	5 Q9Y0W7	Q9Y0W7 drosophila
29	161.5	6.0	1256	11 Q925S5	Q925S5 mus musculu
30	161.5	6.0	1256	11 Q9J1X1	Q9J1X1 mus musculu
31	161.5	6.0	1256	11 Q95T59	Q95T59 mus musculu
32	161	5.9	412	6 QB8T14	QB8T14 oryctolagus
33	159	5.9	650	6 Q9GKR2	Q9GKR2 bos taurus
34	159	5.9	739	6 Q28260	Q28260 canis faml
35	159	5.9	739	6 Q9GKR3	Q9GKR3 bos taurus
36	155	5.7	213	4 QB8W91	QB8W91 homo sapien
37	155	5.7	335	4 QB8CD9	QB8CD9 homo sapien
38	155	5.7	1041	4 Q94856	Q94856 homo sapien
39	155	5.7	1217	11 P97685	P97685 rattus norv
40	153.5	5.7	494	11 Q95SC6	Q95SC6 mus musculu
41	153	5.7	5636	4 Q96RW7	Q96RW7 homo sapien
42	152.5	5.6	373	4 Q9H6B4	Q9H6B4 homo sapien
43	152	5.6	467	4 QB8NR8	QB8NR8 homo sapien
44	151.5	5.6	1151	11 Q9QVN5	Q9QVN5 rattus sp.
45	151.5	5.6	1174	11 Q91260	Q91260 rattus norv

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	623 AA.
QB8Y18			
ID QB8Y18			
AC QB8Y18:			
DT 01-MAR-2003 (TREMBLrel. 23, Created)			
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Weakly similar to stailic acid-binding lectin (Fragmen).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX NCBL_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC SPRAIN=C57BL/6J; TISSUE=Thymus;			
RX MEDLINE=22354683; PubMed=12466851;			
RA The FANTOM Consortium			
RA the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT "Analysis of the mouse transcriptome based on functional annotation of			
RT 60,770 full-length cDNAs."			
RL Nature 420:563-573(2002).			
DR EMBL; AK042488; BAC31272.1; -			
FT NON_TER			
SO SEQUENCE	623 AA;	63384 MW;	5827C09D52C3ACTF CRC64;
Query Match	44.8%;	Score 1211.5;	DB 11; Length 623;
Best Local Similarity	43.1%;	Pred. No. 1.3e-96;	
Matches	267;	Conservative 55;	Mismatches 111; Indels 187; Gaps 8;
QY	2	LLPLLSLIGSQAMDGRFWIVQESVWPBCLICISVPCSFYPRODWTGSPAYGYWF	61
DB	3	LLPLLSLFLDGGOGOMESYFLQVORIVKQDELCIFVPCSFSPGKMKRSLPLGYWF	62
QY	62	KATERTKAPVATFNHOSREVMSTRGRFQDTPKAGNCSTVIRPQAMODESOYPPRVE	121
DB	63	KGTRKPSLSFPVATNNKDKVLEWARKRFQDLDISKNCSTLIKDWQMDSTNYPRME	122
QY	122	RGSYVRYNFMNDGFLLKVTALTKQPDVYIETLEPGQPVVVICVFNAPFECPSPFSWT	181

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Db 123 RG-FERESFKEE-FRLQVEALTOQKPDIFIEVLEPEGPVTVVCLFSWTEQCAPSFSGM 180
QY 182 GAALSSOGKPTTSHFSVLSFTPRPODHDHDLCHVDFSGKYSAAQRYARLVAAPRDL 241
Db 181 GDAVSFOESRPHTSNVSLSFTIPGLQHDHTELTQDLFSR--MSTQRYARLVAAPRDL 238
QY 242 VISISBDN--TRP----- 252
Db 239 AISIFHDNVSVPDLHENPHEVQOGQSLRLCTADSORPATLSWLEOVLSWSSPVGS 298
QY 253 -----PENLRVMSQAQNTVLENG 273
Db 299 RTLALFELPVKAGDSGHYTCQAEENRIGSOQHTLDSLVLXPDLRVYVMSQAQNTVLEELR 358
QY 274 NGTSLFVLEGGSLCTVCTHSSPPARLSTWQGOVLSPSQSDPGLFELPRQVEHEGEF 333
Db 359 NAIISLPVLEGGSLCTVCTHSSPPARLSTWQGOVLSPSQSDPGLFELPRQVEHEGEF 418
QY 334 TGHARHPLGSQHVSLSVHY-----KKGK----- 358
Db 419 TCAAOPLGAORISLSVHYPPQMSPPSCSWEAGLHONCSSRAMPARSLWRIGEGLL 478
QY 359 -----IS 360
Db 479 EGNSSNASTFTVSSLSGPVWNSLSLQELGPSLMLSCESWNTGAGQTTVLLLPDKD 538
QY 361 TAFSNGAFLGIGITALFLCLALIMKILPKRRQOTETPRPRSHSTLIDVINYVPRAG 420
Db 539 TAFSGAVLVGFTITLMLACLIVKTLQKGTGTEBESRPRKLSNGSTILDIYINVPKTR 598
QY 421 PLAKRNOKATPNSRTPLP 440
Db 599 SLA--RNWKAEPDAPSRSP 616

RESULT 2
Q81YH7 PRELIMINARY; PRT; 568 AA.
AC 081YH7:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SIGLEC-like 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxonomy:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035809; AAH35809.1; -.
SQ SEQUENCE 568 AA; 61977 MW; C955F4D62162B860 CRC64;

Query Match 33.6%; Score 909; DB 4; Length 568;
Best Local Similarity 43.1%; Pred. No. 2,3e-70;
Matches 211; Conservative 65; Mismatches 174; Indels 40; Gaps 10;

QY 7 LSLILGSGQANDGFRWIVQSVWVPEGLCTISVPCSFSPRODMGTSTPAYGYWFKVTE 66
Db 110 LSVWVTSQDLSRLREVPESVYVQGLCVSPCSVLVPHYNTASSPVYGSNFKGAD 169
QY 67 TTGKAPVATNHQSEVEMSTRGRFQLTGDPKAGCSLIVRDAQMODESOYFFRVERGSYV 126
Db 170 IPMDIPVATNTPSGKVOEDTHGRFLGDPQTNNCSSISIRDAKRGDSGRKYFQVGEGRS- 228
QY 127 RYFNMDGFLLKATYALQKPDVYIPETLEPGQPVTVICVFNMAFEECPSPSESWTGAALS 186
Db 229 KMWIYIDKLSVHTALHMPFTSIPGLSGHPRNLITCSVPMAECEQPTPTITWMAASVS 288
QY 187 SGTGKPTTSHFSVLSFTPRPODHDHDLCHVDFSGKYSAAQRYARLVAAPRDLVTSIS 246
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Db 289 S--LBPETTRSSMLSLIPQPDHGTSLTCQVTLPGAGVYTMRAVRLNISY----- 336
QY 247 RNDTDPENLRVMSQAQNTVLENGTSLPVLEGGSLCTVCTHSSPPARLSTWQROG 306
Db 337 -----PQNLMTWYFQGDGTASTLRLNGSALSALVLEGGSLHLYCAVDSNPPARLSWTGS 390
QY 307 QVLSFSQSDPGEVLELPRVQVEHEGEFTCHARHPLGSQHVSLSVHYK---KGLISPAF 363
Db 391 LILSPSSQSNLGVLELPRVHYKDEGEFTCRQNPPLGSHISLSLQNEYTKMKRPLISGV 450
QY 364 SNGAFLGIGITALFLCLALIMKILPKRRQOTETPRPRSHSTLIDVINYV--PAG 420
Db 451 TIGARGGAGATLALVFLYCTITFVVY--RSCRKKSARPAVGQDGMEDANAARVGSASOG 507
QY 421 PLAKRNOKATPNSRTPLP--GAPSPESKKNOKKQQLPSPEPKSSTQAPESQSE 478
Db 508 PLI-----SPADSDSPHAPALATPSPSE-----EGELQVSLSFHARAPQYPOQDRA-I 557
QY 479 ELHATLTFP 488
Db 558 GYEYSEINIP 567
```

RESULT 3

Q8BTG2

PRELIMINARY; PRT; 269 AA.

```
AC 08BTG2:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Weakly similar to stalle acid-binding lectin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK036698; BAC29538.1; -.
SQ SEQUENCE 269 AA; 30882 MW; D2D03B384BDA33C5 CRC64;
```

Query Match 24.5%; Score 664; DB 11; Length 269;
Best Local Similarity 55.1%; Pred. No. 1.7e-49;
Matches 129; Conservative 36; Mismatches 65; Indels 4; Gaps 3;

```
QY 2 LILFLLSLILGSGQANDGFRWIVQSVWVPEGLCTISVPCSFSPRODMGTSTPAYGYWF 61
Db 3 LILFLLSLILGSGQANDGFRWIVQSVWVPEGLCTISVPCSFSPRODMGTSTPAYGYWF 62
QY 62 KAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGCSLIVRDAQMODESOYFFRVER 121
Db 63 KGIKRSLSLSPVATNKKQVLEWARGRPQPLGDISKKCSLIRKQVQMGSDTNVFFRME 122
QY 122 RGSYVYRNFMDGFLLKATYALQKPDVYIPETLEPGQPVTVICVFNMAFEECPSPSESWT 181
Db 123 RG-FERESFKEE-FRLQVEALTOQKPDIFIEVLEPEGPVTVVCLFSWTEQCAPSFSGM 180
QY 182 GAALSSOGKPTTSHFSVLSFTPRPODHDHDLCHVDFSGKYSAAQRYARLVAAPRDL 235
Db 181 GDAVSFOESRPHTSNVSLSFTIPGLQHDHTELTQDLFSR--MSTQRYARLVAAPRDL 232
```

```
RESULT 4
Q81W38 PRELIMINARY; PRT; 304 AA.
AC 081W38:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
```


Db 6 LLLPRLLCRGVAKGEKD--YLLTMQSVTVQEGLCVLSFSFYPQDDMTSDPYHGWM 63
QY 61 FRAVETETGAPATVATNHSOREVEMSTRGRFOLTGDPKAGNCSLVIRDAQMDQESQYEFYR 120
Db 64 FRAGDHVSNILVATNTNPAARVRETRDRFHLIGDPQNKDCTLISTDTRSDAGTYEFYR 123
QY 121 ERGSYVRNFMNDGFELKYTA---LTQKPDVYIPE--TLEPGQPVYICV-----FNMAF 170
Db 124 ERGN-1KWSYKHDOQSVNTVATASQDLSRYRLEVEPVQEGLCXVPCSVLPHYNMTRA 182
QY 171 EECPPPSFSW--TGAAL-----SSQGTKPTTSHFVSLSFPPRODHDITLCHV 217
Db 183 SS--PYGSMFKREGADIXMDIPVATNTPSGKVOEDTQGRFLLG---DQTNCSLS--I 235
QY 218 DFRKGVSAO 227
Db 236 RDAKKGDSK 245

RESULT 10
095JN1
ID 095JN1 PRELIMINARY: PRT: 312 AA.
AC 095JN1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 34.6 kDa protein.
OS Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP TISSUE=Testis;
RC Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Sugano S.;
RT Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries.*;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB070150; BAB63095.1; -;
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 34610 MW; 42CA54C314CCLCF0 CRC64;

Query Match 8.7%; Score 235.5; DB 6; Length 312;
Best Local Similarity 24.5%; Pred. NO. 3.6e-12; Indels 103; Gaps 13;
Matches 93; Conservative 44; Mismatches 140;

QY 92 LTGDPKAGNCSLVIRDAQMDQESQYEFYRERGSYVRNFMNDGFELKYTALQKPDVYIP 151
Db 1 MTGNDEDECTLIHILKNGSATYLFYADLGEQ-KSAFLGENIKRLFVSDLTQKPELHP 59
QY 152 ETLPEGQPVYICVFENMAFEECPSPFSWTGAALSSQGTKPTTSHFVSLSFPPRODHDIT 211
Db 60 ETLLEKPAALNCTLTGCTKEIKALFRSRKNPAVSS-----SSSVPHFILRPDHGN 112
QY 212 DLTCHVDSEKRGVSAQRTVLRVAVAPROLVISISDNTPPDENLRVWVSAQNRVLEN 271
Db 113 TLGCHLNFSLANTSSLVKLVQVSPHRLFNSSCS----- 147
QY 272 LQNGTSLPVLEGOSLCLVCTHSSPARLSWTORGQVLSPOSPDPGLE-LPRV----- 325
Db 148 -----LEKTVLC-SCSPHGIPRPSVQMMNG-----VPVDVNSMDNIDPRVSSSTR 191
QY 326 -----QVEHEGEFTCHARRPLDSQHVLSLSVHYKKGLISTAFNSAGFLGT-- 371
Db 192 VPMANSTINLIGPEIYMRLRCEGKNQYGI-HTSSFFLIPNKKV-VSSMFVKLIGIYV 249
QY 372 GITA--LFLCLALILMKL-----KKRRQTPTPRPRSRHSITIIDYIVVYTAGP 421
Db 250 GALAFSLFFCLVLLMKMLNMWEEHQSPKTRKEGLTKRPELLEPEV----- 297
QY 422 LAQKRQKATPNSPTPLPP 441

Db 298 -----PSMFEADIPP 307
RESULT 11
015600
ID 015600 PRELIMINARY: PRT: 430 AA.
AC 015600;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TM2-CEA precursor.
DE BGPI.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP TISSUE=Colon adenocarcinoma;
RC MEDLINE=89139550; PubMed=2537311;
RA Barnett T.R., Kreschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA Elting J.J., Kamarcik M.E.;
RT "Carcinoembryonic antigens: alternative splicing accounts for the
RT multiple mRNAs that code for novel members of the carcinoembryonic
RT antigen family.";
RL J. Cell Biol. 108:267-276(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.M.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala M., Terry A., Barnes J.,
RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Andrade T., Frankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Ariellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: X14831; CAA32940.1; -;
DR EMBL: AC004785; AAC18435.1; -;
DR InterPro: IPR001589; Actbind_actnln.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000920; Myelin_P0.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00213; MYELINP0.
DR SMART: SM00408; IGC2.1.
DR PROSITE: PS00019; ACTININ.1; 1.
DR PROSITE: PS50835; IG_LIKE.2.
KW Alternative splicing; Immunoglobulin domain; Signal; Transmembrane.
FT SIGNAL 1 34
FT CHAIN 35 430 POTENTIAL.
SQ SEQUENCE 430 AA; 46910 MW; 195DE9F17D1D1414F CRC64;

Query Match 7.6%; Score 205; DB 4; Length 430;
Best Local Similarity 22.6%; Pred. NO. 2.5e-09; Indels 178; Gaps 29;
Matches 124; Conservative 73; Mismatches 174;

QY 5 LLLSLILGSGQAMDGKFWIRVQSVVAPRGLICVSP-----CSFSYPRODWTGSTPAY 57
Db 19 LILASL-----TFMNPPTTAQLTTESMPNVAEGKEVLLVHNLPQO-----LF 63
QY 58 GY-WFRAVETTKGAPVATNHSOREVEMSTRGRFOLTGDPKAG-----NCSLVIRDAQ 109
Db 64 GYSWYKG--ERYDG-----NRQIVGAIGTQATTPPANSGRETIYPNASLILQNTY 113
QY 110 MODESQYFVRERGSYVRNFMNDGFELKYTALQKPDVYIPELTPGQPVYICVFNMA 169
Db 114 QNDTGYTTLQV-----IKSDLVNE-----EATGQPHYV----- 141
QY 170 EECPPPSFSWTGAALSSQGTKPTTSHFVSLSFPPRODHDITLCHVDFSRKGVSAQRT 229

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Db 142 -PELKPSP-----ISSNNSNPVEDKAV-AFTCEPETQDTYTLWMINNOISLPVSP--- 189
OY 230 VALRYAYAPRL-VISISRDNTDPDENLRVWQANRP--VLENIAGNTSLPVE----- 282
Db 190 -RLQISNCRITLTLSVTRNDGPECEIQNPVS-ANNSDEPTLVNTGPTPTTSPSPT 247
OY 283 ----GOSICLVCTVTHSSPPARLSWTQROVLSPSQSPDGVLELRVQVEHEGEFTCHAR 338
Db 248 YRRPQANLISLCYAASNPAPQYSWMLNGTFQOSTOE-----LFINPTVNNNGSYTCAN 302
OY 339 HPL-GSOHVSLSVHYKKGL-ISTAFSNGAFLG--IGITALELCLALLIKTL----- 389
Db 303 NSVTCNCNRTYKTIIVTDNALPQENGSLPAGIYGVVALVAL-LVALACFLHEGKT 361
OY 390 ---PARRTOTETPRPRFSRHSITLIDYINVPYAGPLAQRKQKATPNSPRTPLPPGASP 446
Db 362 GRASDQDRLTE-HKPSVSNHTQ--DHSN-----DP 388
OY 447 ESKKQKQKQYOLPSPPEKSSQAPESQSEELHYATLNPQVAP-RPEARMRK--GTQ 503
Db 389 PKKN-----EVTYSLNFEADQPTQPSASPLTATE 421
OY 504 ADYAEVKFO 512
Db 422 IYSEVKKQ 430

RESULT 12
O9D4M0 PRELIMINARY: PRT: 367 AA.
ID Q9D4M0:
AC Q9D4M0:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 4931406B18Rik protein.
GN 4931406B18Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli I., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontaiki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016431; BAB30231.1;
DR MGD: MGI:1921304; 4931406B18Rik.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PSS0835; IG_LIKE; 1.
SQ SEQUENCE 367 AA; 40625 MW; 24CANDEA63F47F95 CRC64;
Query Match 7.3%; Score 198.5; DB 11; Length 367;

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Best Local Similarity 23.5%; Pred. No. 7.5e-09;
Matches 102; Conservative 65; Mismatches 146; Indels 121; Gaps 22;
OY 1 MLPL-LTSLGSGQAMDCRFWRVQDSVAVPBGCLISVPCSSYPRQDWTGSTPAYCY 59
Db 9 LLLYLGLISPLV-----VDYKKTAM-EDGLSMVPCVIEF----- 42
OY 60 WEKAVETTKGAPVATNHSREVMSTGRFLQGDPA--KGNCSLYIRDAQMODESQYE 117
Db 43 -YKAPFRN-----PAVSTRINE-NISFRVG---ISHSAPMGDIS-----TEEVEYC 85
OY 118 FRVERGSYVRYNEMNDGFEIKVTA--LTQKPDVYIPETLEPGQPVTVICVFNNAFECR 174
Db 86 ILMTN-SMLRRKRYMNSLYVLGCTQKDLTONPELHIESSVAGBPVLTSTIGTQCEPN 144
OY 175 PPSFGMGALSSQGT---KPTSHFVLSSTPRPOHDHDLQCHVDPSKRGVNAQTVR 231
Db 145 ALFLSMKGPIMSSMTTTSIHPS---SALATELPEQGTTLRCHLKLSDLDNLSKRVK 200
OY 232 LRVAAPRDVVISISRDNTDPDENLRVWQANRVLENIGNTSLPVEGOSLCLVCV 291
Db 201 LQVSPPTRLNYS-----CLKRTLQSCS 225
OY 292 THSSPPARLSWTQROVLSQSPDGVLELRVQVEHEGEFTCHARPLGSOHVSLSL 350
Db 226 FHGIPTPLVQWVGTFVSVNRID--GILHITTTTLE---PWTNSTIHLIWEPRILTLR 280
OY 351 -----SVHYK-----GLISTAFSNGAFGI---GITALELCLALLIKTL--- 389
Db 281 CEGKNQYGVHASFRLPLPDKSSVSVFLRGLIGIYGAISALFLFVLVVKMLMW 340
OY 390 PKRRT--QTEPRP 401
Db 341 EENQTCNKKEAPTP 354

RESULT 13
ID Q13854 PRELIMINARY: PRT: 461 AA.
AC Q13854;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Biliary glycoprotein.
GN BGP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89139550; PubMed=2537311;
RX Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA Eiling J.J., Kamarck M.E.,
RT "Carcinoembryonic antigens: Alternative splicing accounts for the
RT multiple mRNAs that code for novel members of the carcinoembryonic
RT antigen family.";
RL J. Cell Biol. 108:267-276(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA KUROKI M., Matsuo Y., Misumi Y., Oikawa S., Matsuo K.Y.;
RT "A new isoform of human biliary glycoprotein (BGP) containing a domain
RT encoded by an Alu-like sequence.";
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: D12502; BAA02063.1;
DR InterPro: IPR001589; Actbind_actnln.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00408; IgC2; 1.
DR PROSITE: PSS00019; ACTININ_1; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.

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RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21560925; PubMed=11544254;
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4, a new afadin-associated member of the nectin family
that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 276:43205-43215(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC024948; AAH24948.1; -
DR EMBL: AF472510; AAL7983.1; -
DR InterPro: IPR007110; I9-1like.
DR InterPro: IPR003598; I9-C2.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9_2.
DR SMART: SM00408; I9C2; 1.
DR PROSITE: PS50835; I9_LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 508 AA; 55657 MW; 24DAEBD21F22E376 CRC64;

Query Match 6.9%; Score 186.5; DB 11; Length 508;
Best Local Similarity 21.6%; Pred. No. 1.3e-07;
Matches 115; Conservative 70; Mismatches 211; Indels 137; Gaps 25;

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QY 46 PROD-----WTGSTPAYGWFKAVETTTKGAIVATNHQSEVENSTGRFQLTGDP 96
DB 54 -RGPDDEQVGVAVARVDNPEGIRRELALHSHKYGILHVPAYEDR-VEQPPPP-----DP 106
QY 97 AKGNCSLYIRDAQMDQESQYFFVRERGSYVRYNFMNDGFLKAVTALTKQKPDVYIPETLEP 156
DB 107 LDG--SYLNRNAVQADGEGYECRVS-----TFPAGSFQARMRLRYLVPL--PSLNP 154
QY 157 GQPYT----VICVENMAFECCPPPSFSW---TGAALSSQGTKE---TTSFVSLSFTP 204
DB 155 GPPLIEGGGLFLASCAEGSPAPSVMTDEVKGTQSRSFTHRSAAVTSFHLV--P 211
QY 205 RPQDHDTLTCGVDFSRKGVSAQR--TVRLKVAIAPRDLYVISRDNTDPDENLRWVS 262
DB 212 SRSNMGQPLTCVV--SHPGILLQDRRITHTLQVAFLEASVRLDQN----- 256
QY 263 QANRTVENLNGNSLVLBGSQSLCYVTHSSPPARLSWTQRGVLSPSQSPDPVLEL 322
DB 257 -----LMQYGR-----EGAT--LKCLSEGQPPPKYNMWTRLDGPLPSGVRYKGDYLG 301
QY 323 PRVVEHEGEFTCHARPLGSHVLSLV-----HYKKGLISTAFSNGAFLGITAL 376
DB 302 PPLTEHSGYVYCHVSNELSRDSQVVEVLDPEDPGQYDLVS-----ASVITVGYIAA 356
QY 377 LFLCLALILKILPKRRTQETPRPRFSRSHSTIADYINNVFTAGPLAQRNQAAT---PN 433
DB 357 LFLCLLVVVVYLM-----SRYHRRK-----AQOMTKYEELTLTREN 394
QY 434 SPRTPLPPGAPSPESKKNOKQYQLPSFPP--KSTQAPESQSEELHYATL 485
DB 395 SIRR-LMHSHPSPQPEESYGLRAEGHPDLKDNSSCYWSEPEGRSYSTL 446

Search completed: October 8, 2003, 20:03:11
Job time : 68 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2003, 20:01:08 : Search time 23 Seconds
(without alignments)
941.876 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	888	32.8	431	3	US-09-038-832-2
2	888	32.8	431	3	US-09-038-832-4
3	831.5	30.7	467	3	US-09-046-736-2
4	769	28.4	440	3	US-08-759-628-4
5	693.5	25.6	421	3	US-08-759-628-5
6	573	21.2	374	3	US-09-046-736-4
7	177.5	6.6	501	2	US-08-408-095-31
8	172.5	6.4	403	4	US-09-638-649-5
9	167	6.2	464	2	US-08-602-725-32
10	155	5.7	321	6	516835-17
11	153.5	5.7	416	4	US-09-638-649-1
12	152.5	5.6	373	4	US-09-996-243-503
13	151.5	5.6	1241	3	US-09-040-774-2
14	143	5.3	642	1	US-08-217-299-1
15	143	5.3	698	2	US-08-602-725-36
16	143	5.3	734	2	US-08-389-459A-17
17	143	5.3	734	2	US-08-987-867A-17
18	139.5	5.2	611	2	US-08-752-307B-10
19	139.5	5.2	611	4	US-09-707-802-10
20	139.5	5.2	611	4	US-09-991-326-10
21	139	5.1	404	4	US-09-638-649-3
22	138	5.1	354	6	516835-4
23	136.5	5.0	432	4	US-09-778-510-2
24	136	5.0	1091	3	US-08-986-485-5
25	135.5	5.0	630	2	US-08-752-307B-14
26	135.5	5.0	630	4	US-09-707-802-14
27	135.5	5.0	630	4	US-09-991-326-14

28	134.5	5.0	398	4	US-09-778-510-6	Sequence 6, Appl
29	132.5	4.9	972	3	US-08-750-141A-2	Sequence 2, Appl
30	132	4.9	647	5	PCT-US93-00031-23	Sequence 2, Appl
31	132	4.9	828	1	US-08-261-304-2	Sequence 2, Appl
32	131.5	4.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
33	130.5	4.8	946	5	PCT-US95-08493-13	Sequence 13, Appl
34	130	4.8	408	4	US-09-724-864-62	Sequence 62, Appl
35	129	4.8	612	2	US-08-359-705B-8	Sequence 8, Appl
36	129	4.8	612	2	US-08-286-846A-8	Sequence 8, Appl
37	129	4.8	612	2	US-08-457-880A-8	Sequence 8, Appl
38	129	4.8	612	3	US-08-444-622A-8	Sequence 8, Appl
39	129	4.8	612	3	US-08-942-562-8	Sequence 8, Appl
40	129	4.8	612	3	US-09-156-923-8	Sequence 8, Appl
41	129	4.8	739	4	US-08-482-073-6	Sequence 6, Appl
42	129	4.8	739	5	PCT-US93-00031-9	Sequence 9, Appl
43	129	4.8	839	2	US-08-359-705B-6	Sequence 6, Appl
44	129	4.8	839	2	US-08-286-846A-6	Sequence 6, Appl
45	129	4.8	839	2	US-08-457-880A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-038-832-2

Sequence 2, Application US/09038832

Patent No. 6146845

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: ERICKSON-MILLER, CONNIE

TITLE OF INVENTION: Staloachdesin Family Member-2

TITLE OF INVENTION: (SAF-2)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA

STREET: P.O. Box 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED for Windows Version 2.0

CURRENT APPLICATION DATA:

Query Match 32.8% Score 888; DB 3; Length 431;

Best Local Similarity 47.8%; Pred. No. 9.8e-70;
Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;

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0Y 1 MLPLLLLSLLSGQANDS-----RFRVROQESVAVPBGCLSTVPCSESTVPRODMTGST 54
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Db 1 MLMLLLLPMLLMTGKKGHEGROYGDGYLL:LOVELYVBOGLCVHNPSCFSYPODGMOTSD 60
    | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
0Y 55 PAVGYWPKAVTETTKGAPVATNHQSEVEKSTRGFRFOLGDPKANGCSLYVRDQM0DES 114
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Db 61 PVHGUYWRADDRYQDAPVATNNPDEVOAETGROFOLLGIDWMSDSCSLTRDAKKRKG 120
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
0Y 115 QYFFRVRGSGY-----VRVFNMDGFFLVTALATOKPDDVYIPETLEPQOPVTVLCVFNMA 165
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Db 121 SYEFLRERGGSMKMSYKSQNLNYKTKOLSVFVTLATHRPDLILGLTLESHSNLNCVPMWA 180
    | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
0Y 170 FEECPPESEFSGTAALISOGTKPTTSHSEVLSFTFRPODHDITLCHVDSRRKGVSAORT 229
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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RESULT 2
 US-09-038-832-4
 : Sequence 4 Application US/09038832
 : Patent No. 6146845
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 : GENERAL INFORMATION:
 :
 : APPLICANT: KIKLY, KRISTINE
 : APPLICANT: ERICKSON-WILLER, CONNIE
 : TITLE OF INVENTION: Sialoadhesin Family Member-2
 : TITLE OF INVENTION: Sialoadhesin Family Member-2
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: RATNER & PRESTIA
 : STREET: P.O. BOX 980
 : CITY: VALLEY FORGE
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19482
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : OPERATING SYSTEM: IBM compatible
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/038,832
 : FILING DATE: 11-MAR-1998
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/041,886
 : FILING DATE: 02-APR-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PRESTIA, PAUL F.
 : REGISTRATION NUMBER: 23,031
 : REFERENCE/DOCKET NUMBER: GH-50018
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 610-407-0700
 : TELEFAX: 610-407-0701
 :
 : TELEX: 846169
 :
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 431 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 :
 : MOLECULE TYPE: protein

US-09-038-832-4

Query Match	32.8%;	Score 888;	DB 3;	Length 431;
Best Local Similarity	47.8%;	Pred. No. 9,8e-70;		
Matches 195;	Conservative 52;	Mismatches 127;	Indels 34;	Gaps 6

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QY      MLPLILLSLIGSSQAMDQ-----RFTWROEVSVMPEGLCISVPGSEFVPRDDMGST  54
Db      1 MLLLLLLLPLMNTKMEGDROYGDBYLLQVQVELYTVQEGICLVHVCFSFTPDQWMDSD  60

QY      55 PAYGVFKAVETTKGAPVATNHQSEVEEMSTGRFRLOTGDPKANCSLVIRDAQODES  114
Db      61 PVHGVMFRAGDRPYQDAPVATNNPNDBREVQAEITGRFOGLLDGIMSDCLSTIRAKRRDKG  122

QY      115 QYEFVRERASY-----VRYNEMODGFEFLKVTALTOCKPDVYIPELIEPQPYTVICVFNMA  165
Db      121 SYEFLERESMKMSKYSKQSLNRYTKOLSEFVVALTHRPDILLIGLESGSHNLGCSAPMA  180

QY      170 FEECPPEPSMTGGAALSSQGTKPTTSHFSVTSFTRPDHDJDTLCHVDESRKCVSART  222
Db      181 CKQGTPEPLMSWIGASVSSPG--PTTARSSVLTLPTRKPDQHTSLTCQVTLTGCTVVTYTT  238

QY      230 VRLRAYAVRDLVISTSRDNPDPPEPENTRVMSQANRTVLENLNGTSLPYLEGOSICLV  289
Db      239 VRLDVSY-----PPMNLTMVFEQDADATAPALDNGSSLVLTBEGOSLRV  282

QY      290 CVTHSSPPARLSWTQROGVLSQSDSDGVLELRVQVYEHMGEGTTCAHRHPLSGHVSLS  349
Db      283 CAVNSNPPARLSWTGSLTLCEPSRSSNGELLEPRVHRDEGEFTTCAQNAQNGOSHISLS  342

QY      350 LSVHYKGLISTAFNSN---GAFGLIGTIFALLFL---CLALIMTKLTPKR  392
Db      343 LSLQNEGIGTSPRVSQVTLAAVGGAGATLAFELSPCLITFIITVRSCKRK  390

```

RESULT 3
 US-09-046-736-2
 : Sequence 2, Application US/09046736
 : Patent No. 6090582
 : GENERAL INFORMATION:
 : APPLICANT: KIKUY, KRISTINE
 : APPLICANT: ERICKSON-MILLER, CONNIE
 : TITLE OF INVENTION: Staladhesin Family Member-3
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Ratner & Prestlia
 : STREET: P.O. Box 980
 : CITY: Valley Forge
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19482
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/046,736
 : FILING DATE: 24-MAR-1998
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/041,885
 : FILING DATE: 02-APR-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Prestlia, Paul F
 : REGISTRATION NUMBER: 23,031
 : REFERENCE/DOCKET NUMBER: GH-50019
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 610-407-0700
 : TELEFAX: 610-407-0701
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:

```

:      LENGTH: 467 amino acids
:      TYPE: amino acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:
US-09-046-736-2

```

Query Match	30.7%;	Score 831.5;	DB 3;	Length 467;
Best Local Similarity	37.9%;	Pred. No. 1e-64;		
Matches 198; Conservative	78;	Mismatches 174;	Indels 73;	Gaps 11;

OY	2	LLPILLSLLGSSQAMDR-----FWLRVQSVWVPGALCISVGCFSYPRDMWTSP	55
OY	1	MLLLLLLPLMREVEGOKSMRKXOYSLTLMSSVTVQDGKMHVHRCFSFYVDSQTSDP	60
OY	56	AVGYEFKAVETTKCAPVATNHQSFVEWEMSTRGRFOLTGRPAKNCSLVTRDAQODESQ	115
OY	61	VHGVEFRACNDISMARPAVATNPPAWAOEELRDFRHLGDPOTKNCTLSIRDAHMSDAGR	120
OY	116	YEFVRGCVSVYVRNMMNOGFLLKVALQKRPDVYIPELLEBGOVTVLCVFNMAFEBCRP	175
OY	121	YEFREMEKGN-IKMVKKYDOLSVNTYALTHHRNILLPTGLESGCQNLTCSPYACAEQGT	179
OY	176	PBSWTGAALSSQGTFRPTTSHFSVLSFTPRRODHTDLTCHVDSRKQVSAQFTVRLVA	235
OY	180	PMISWKGTSVSR--PHPSYTRSSVLTLLPQFQHNHTSLTCVYLPAGAVTYTNTIOLNVS	237
OY	236	VAPRODLVISISNDTPRPNELRVWVSQANFTVLENGSLLELEAGOSLCIVCYTHSS	295
OY	238	Y-----PPQNLTVYVFOGEGTASTALGNSSSLSVLEBQSLRLCAVDNS	281
OY	296	PARLSWTRQGVLSPSQSPDQVLELPRVOVEHEGEFTCHARRPLGSOHVSLSLVHYK	355
OY	282	PARLSWTRSLTLTPSQSPNPLYEL-QVHIGDEGEFTCAQNSLSDSHVSLSLDQE	340
OY	356	-----KGLSTAFNSCAPLGLGIGITALLFLCLALLIMKLPPRRKROTEPRPRRSRHS	407
OY	341	YTGKMRPVSGVLL-----GAVGAGATALVELSPCVLFTV--RSCKRKSARP-----	386
OY	408	TILDYINVPYTPAGLPAQRNOKATPNPSDPTLPFGAGSPESKSNOKOYOYLPSFPEKSS	467
OY	387	-----AADVGDMK-----DANTIRGSASQGNLTESMADNPRHH	422
OY	468	TOAPESQESQELHATATINPGVVRPRPARMPKGTQADYAAVYK	510
OY	423	GLAHSNGEEREIOYALPSFKHGEQO-DLSCQDEATNNEYSIK	464

RESULT 4
 US-08-759-628-4
 Sequence 4, Application US/08759628
 Patent No. 6225446
 GENERAL INFORMATION:
 APPLICANT: Altmann, Scott W.
 APPLICANT: Rock, Fernando L.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,628

```

1          CLING DATE: 05-DEC-1996
2          CLASSIFICATION: 435
3          PRIOR APPLICATION DATA:
4          APPLICATION NUMBER: US 60/008,574
5          FILING DATE: 06-DEC-1995
6          ATTORNEY/AGENT INFORMATION:
7          NAME: Ching, Edwin P.
8          REGISTRATION NUMBER: 34,090
9          REFERENCE/DOCKET NUMBER: DX0552Q
10         TELECOMMUNICATION INFORMATION:
11         TELEPHONE: 415-855-9196
12         TELEFAX: 415-496-1200
13         INFORMATION FOR SEQ. ID NO.: 4:
14         SEQUENCE CHARACTERISTICS:
15         LENGTH: 440 amino acids
16         TYPE: amino acid
17         STRANDEDNESS: single
18         TOPOLOGY: linear
19         MOLECULE TYPE: protein
20         US-08-759-628-4

```

Query Match	28.4%;	Score 769;	DB 3;	Length 440;
Best Local Similarity	36.5%;	Pred. No. 2.8e-59;		
Matches 190;	Conservative 73;	Mismatches 163;	Indels 94;	Gaps 15;

QY	1	LPRLSSLLSGQADNGFIRWQSVSWPVGGLISVCSGF--SYPRDWTGCTPVYGV	59
QY	2	LPRLSSLLSGQADNGFIRWQSVSWPVGGLISVCSGF--SYPRDWTGCTPVYGV	59
Db	1	MLPRLPLPLMAGALMGRERFQLEGPESLIVQGGCLVPLCPALPTLP-----ASYTGCV	55
QY	60	WFKAVTETTKGA--PVATNHQSEVEMSTGRFQLTGDPKAGNCSLVTRQAMODESQYF	117
QY	118	FREREGSYRYNFMNDGFELKYATLTQKRDVYIPELTBEG--QPVTVCYVNAFEECPR	175
Db	56	WF-----LEGADVPVATNDPDEEYQEEGRFGFLHMDPRKKNCSLIRDARRDNAYF	109
QY	110	FRL-KSKMMKYGTSSKIVYRWALTHRPNISIP--GPGWPSSNLITGSVPWVCEQTP	165
QY	176	PSEFWMGAAALSSQGTPTTSHFSVLSFTPRQDHTDITLCHVDESRKVSQORTVRLVA	235
Db	166	PLSWMNAPRHLLG--PRTTQSSVLTIR-AQDHTNLTCQVTFPGAGVTHMERITQLNVS	222
QY	236	YAPRDLVISISRDNPDPENLRVWVSQANRTVLENLGNLSPLVBSQSLCLVCVTHSS	295
Db	223	YAAQKVAISIT-----FQNSNAFKIILONTSSLPLLEQOALRLICDADGN	266
QY	296	PPARLSMTQRGQVLSQPSPDPGVLELPYQVQEHGGEFTCARHPHLSQSHVLSLSVHYK	355
Db	267	PPAHLMSFQASPPXNPTPISTNGVLELPQVSGAEBGDTTCRAQHPGLSQLSLSLFWHMK	322
QY	356	K-----GLISTAFNSNGAFGLIGITVLLFLCLALIMLKILPRRTQTEPRPRFSRHSITL	410
Db	327	PEGRAGVL-----GAWMGASITLTVLFCVCFIR-----RVTRKRKKQPSQCKXT	371
QY	411	DYINNVPTVAGPLAQRKQKATPNSPRTLPGCAPSPESKKQKKQYQYLPSPPEPKSSTQA	470
Db	372	DDVNPMPWVS-----SRGHQHFOTGEIVSDHPAEA	401
QY	471	PESQSEDELHATVLTNFGVRPRPEARMPKGTQADYAEVK	510
Db	402	GPISDEQDELHATVLTNFGVRPRPEARMPKGTQADYAEVK	437

RESULT 5
 US-08-759-628-5, Application US/08759628
 : Sequence 5, Patent No. 6225446
 : GENERAL INFORMATION:
 : APPLICANT: Altmann, Scott W.
 : APPLICANT: Bazan, Fernando L.
 : APPLICANT: Kastelein, Robert A.
 : TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 : NUMBER OF SEQUENCES: 11

RESULT 5
 US-08-759-628-5
 Sequence 5, Application US/08759628
 Patent No. 6325446
 GENERAL INFORMATION:
 APPLICANT: Altman, Scott W.
 APPLICANT: Rock, Fernando L.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Kasteleijn, Robert A.
 TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 NUMBER OF SEQUENCES: 11

```

CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX05520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-759-628-5

Query Match      25.6%  Score 693.5; DB 3; Length 421;
Best Local Similarity 43.0%; Pred. No. 11e-52;
Matches 157; Conservative 53; Mismatches 132; Indels 23; Gaps 4;

QY 3 LPLLLSL- GGSQAMDGRFWIRVOESYVWVEGLCISVPCSFSPYRQDWTGTPAYGYWF 61
   :||| | | | | : :||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MLLLLPLLMGSSLDKRPVYELQVKSTYQEGLCVLPCSTSYWRMYSSPLYTWYWF 60
QY 62 KAVTTTGAPVATNHOSEYEMSTRGRFQLTGDPKNCSTVTRDAOMODESOYFFRYE 121
   :||| | | | | : :||| | | | | | | | | | | | | | | | | | | | | | |
Db 61 RDGEIPYAEVVAATNPNRVRKPTQGRFRLGDVOKKNCSTLIGDAMHEDTGSYFFRYE 120
QY 122 RGSYRVNFMNDGFFLKVTALQKPDVYIPELTLPG--QPYTVICVFWMAFEBCPPSFS 179
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 RGRDVKYSQNKMLNLETALIEKPDHLSGPLSGLMKPTRLSCSLPGSCVAGPILTF 180
QY 180 WTGAALSSQGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGVSAQRTVRLRAVAPR 239
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 WTGNAXSAPWT-PPXAPRELTLTPREDHGTNLTCQKRGQAQVTTETXQVLNVYAPQ 239
QY 240 DLVISISDNTPPDPENLRVWVSQANRTVLENLNGTSLPYLEQSLCLVCVTHSSPPAR 299
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 TITTF-----RNGIALEIILQNTSYLPYLEGOALRLLCDADSPNPAH 280
QY 300 LSWTORGVLSPPSDPGVLELPRVOYEHGEFTCHARHPLGSOHSLSYHYKKGGLI 359
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 281 LSWRQGSALNATATISNTGILKRVKSAEBGGFTCAQAHPLGLQIFLNLVSYPDL 340
QY 360 STAFS 364
Db 341 GPSCS 345

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```

APPLICANT: KIKLY KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-046-736-4

Query Match      21.2%  Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 3.6e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166; Gaps 10;

QY 2 LPLLLSLGGSQAMDGR-----FWIRVOESYVWVEGLCISVPCSFSPYRQDWTGTP 55
   : | | | | | | | : : | | | | | | | | | | | | | | | | | | | | | |
Db 1 MLLLLPLLMGRERIVMOKSNRKDYSLTMQSVTVQEGMCVHRCFSYVDSQTDSDP 60
QY 56 AYGYWFAVYETTGAVATNHOSEYEMSTRGRFQLTGDPKNCSTVTRDAOMODESQ 115
   : | | | | : : | | | | | : : | | | | | | | | | | | | | | | | |
Db 61 VHGWFRAQNDISKAKAVATNPNRVAWQETRDFHLSDPQTKNCTLSIRDAKMSDAGR 120
QY 116 YFRFVEGSAVRINFMNDGFFLKVTALQKPDVYIPELTLPGGQPVTVICVFWMAFEBCPP 175
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 YFRFMERGN- IKWYKQDQLSVNVTY----- 145
QY 176 PSFSWTGAALSSQGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGVSAQRTVRLRAVA 235
   || | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 ----- 145
QY 236 YAPRDVLSISRNTDPPDENLRVWVSQANRTVLENLNGTSLPYLEQSLCLVCVTHSS 295
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 -----PPQNLVTVTFQGGSTALNGSSSLSYLEGGSLRLVCAYVDSN 188
QY 296 PPARLSWTORGVLSPSDPGVLELPRVOYEHGEFTCHARHPLGSOHSLSYHYKKGGLI 355
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 189 PPARLSWTMRSLTLXPSQSNPLVLEL-CVHLGDEGEFTCAQAHPLGLQIFLNLVSYPDL 247
QY 356 -----KGLISTARNSGAFIGITALLFLALILIMKILPKRTQETETPRPRSRKS 407
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 248 YTKKMPVSGVLL-----GAVGAGATVATLVSFCVITFV--RSCRKKSAP----- 293
QY 408 TILDYINVTAGPLAQKRNOKATPNSPRTPLPGAPSPESKKNOKQYQLVSPFEPKSS 467

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RESULT 6
US-09-046-736-4
Sequence 4, Application US/09046736
Patent No. 6090582
GENERAL INFORMATION:

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Db 294 -----ADVDIDMK-----DANTINGSASOGUFTSMADPNRHH 329

OY 468 TQAPESQSEELHYATLNPCVRRPEARMPKQTADYAEVK 510

Db 330 GLAAHSSGERETQVAPLSPHKGEPQ-DLSGQATNNEXSEIK 371

RESULT 7

US-08-408-095-31

; Sequence 31, Application US/08408095

; Patent No. 585678

; GENERAL INFORMATION:

; APPLICANT: Chinadural, Govindaswamy

; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MTON, ZINN, MACPEAK & SEAS

; STREET: 2100 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/408,095

; FILING DATE: 21-MAR-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mack, Susan J.

; REGISTRATION NUMBER: 30,951

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)293-7060

; TELEFAX: (202)293-7860

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-408-095-31

Query Match 6.6%; Score 177.5; DB 2; Length 501;

Best Local Similarity 20.0%; Pred. No. 2.8e-07;

Matches 107; Conservative 82; Mismatches 182; Indels 165; Gaps 24;

OY 25 VQESVAVPGLCTSVPCSF-----SYPRDDMTGSTPAYGWPKAVTETTKGAPVATNHOS 79

Db 80 IQMPPIREGDVTYLCNTNNSNPSVTRTEM---KPHGAMEPSSLGVLITQNVGDMNTT 135

OY 80 REVENSTRGRFOLTGDPARGNCSLYIRDAQOMODESOYFFRVERGYSVYRNFMDGFLKY 139

Db 136 --TACARCNSMCSMASPVALNVQYAPRDVRR-----KTL 167

OY 140 TALTORPDYIPTLEPGQPVYIYICFNNAFEECPSPSSW--TGAALSSQGTPTTSHF 197

Db 168 KPLSE-----HSGNSVSLQCDPSSHPK--EVOEFWEKNRGLG---KESQNLN 212

OY 198 SVLSFTPRPODHTDLCCHVDFSRKGVSAQRTVRLRAVAPRDLVISISRDNPDPDENL 257

Db 213 DSI-----PEDAGS-YSCWVNNIS-ICOTASKANTLLEVLAAPRLRVSMSFGD----- 258

OY 258 RVNVAQANRTVLNENLNGTSLPYLEGOISLCLVCVTHSSPPAR-----LSWTORGOVLSPSQ 313

Db 259 -----QVMEGKSATLTCESDANPVPVSHYTWFDMMNQ-----SL 291

OY 314 PSDPGVLELPRVOVEHEGEFTCHARRPLGSOHVSLS-LSVHYKKGLISTAFSGAPLGIG 372

Db 292 PHSORLRLPEVVOHSGAVWCQGTNSVGKRSPLSTLTIVYSPETI-----GRRVAVG 345

OY 373 ITALLFLCALIIMKI-----LPKR--RTQET-----PRPRFSRHSTIIDYIN 414

Db 346 LGS-----CLATILALICGLKLORRWKRTQSOGLQENSQSFVFRNKKVRAAPLISGPH 401

OY 415 VPTAPPLAQRNOKATPNSPRTPPLPGAPSPSK-----KNOKROY 456

Db 402 SLGCYNPMMEDGISYTLTRFPEMNIPRTGDAESEMQRPPRTCDQVTVYSAHKROYGDY 461

OY 457 Q--LPSPPEPKSTQAPESODELHYATLNPCVRRPEARMPKQTADYAEVK 510

Db 462 ENVIPDFPE-----DEGIHYSLEIOFGVERPOAQ-----ENVDYILK 500

RESULT 8

US-09-638-649-5

; Sequence 5, Application US/09638649

; Patent No. 6563015

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Schmidt, Ann Marie

; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED

; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

; FILE REFERENCE: 0575/62175

; CURRENT APPLICATION NUMBER: US/09/638,649

; CURRENT FILING DATE: 2000-08-14

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Murine

US-09-638-649-5

Query Match 6.4%; Score 172.5; DB 4; Length 403;

Best Local Similarity 23.3%; Pred. No. 5.7e-07;

Matches 101; Conservative 46; Mismatches 139; Indels 147; Gaps 21;

OY 100 NCSLYIRDAQOMODESOYFFRV--ERGSYVRNFMNDGFLKYATLQKPDVYIPET-LEP 156

Db 80 NCSLLPATGIVEGTFRCRATNRKGEKSNVR---VRVQIPGKPEIIVPASLTA 134

OY 157 GQPVTV-ICVFNNAFEECPSPSSW--TGAALSSQGT-----PTSHSPVLS-F 202

Db 135 SVPNKVGTCVSEGSY--PAGTSLMHLGKLLIPDGKETLVKEETRRRHPTGLFTLSSEL 191

OY 203 TPAP-ODHDITDLCCHVDFSRKGVSAQRTVRLRAVAPRDLVISISRDNPDPDENLRVNV 261

Db 192 TVIPTGCGTTHPFSCSFS-LGLPRRRPLNT---APIQ-----RVREPGPEGLOLV 241

OY 262 SQANRTVLNENLNGTSLPYLEGOISLCLVCVTHSSPPARLSWTORGOLVSPSPSDPVYLE 321

Db 242 EPEGGI-----VAPGCTVLTCAISAQPPQVIMKIDAPL-PLAASP--VLL 286

OY 322 LPRVOVEHEGEFTCHARRPLGSOHVSLSVHY-----KGLISTAFSNGA 367

Db 287 LPEVGHADGETYSCVATHPSHGPOESPVSIRVTEGDECPAGSVGESGLTALALGI 346

OY 368 FLGIGITALLFLCALIIMKILPKRRTOTETPPRFRSHSTIIDYINVPTAGPLAOKRN 427

Db 347 LGSLGVALL-----VAILMKR 365

OY 428 QKATPNSPTPLPPGAPSPESKNOKKOYQLPSFPEPKSSTQAPESODELHYATLN 487

Db 366 Q-----PREERK-----APESEODEE--RAELN- 388

OY 488 PGVRRPEARMPK 500

Db 389 ----QSEEAEMPE 397

```

RESULT 9
US-08-602-725-32
; Sequence 32, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DUBBIN, HEIDA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-602-725-32

Query Match      6.2%; Score 167; DB 2; Length 464;
Best Local Similarity 23.5%; Pred. No. 2.1e-06;
Matches 85; Conservative 52; Mismatches 122; Indels 102; Gaps 18;

QY 5 LLSLSLGGSGAANGRMIRQESVMPEGLICISVP-----CSFSYPRQDWTGSTRPAY 57
  ||:|||||
DB 19 LITIASL-----TWNPTTAQLTTESMPFVAGKEVLLVHMLPQ-----LF 63
  ||:|||||

QY 58 GY-WFKAVETTTKGAPVATNHSREVMSTRGRFOLGDPAGK-----NCSLYIRDAQ 109
  ||:|||||
DB 64 GYSWYKG--ERYVDG-----NQIYGAIGVQOATPGFANGSGRETIYFNASLLIONVT 113
  ||:|||||

QY 110 MDESQYFFERYKESYRYNFMNDGFLLKVTALTOKPDVYIPTLEPGQPVTVICVFNMA 169
  ||:|||||
DB 114 QNDTGFYTLQY-----IKSDLVNE-----EATGPFHY-----141
  ||:|||||

QY 170 FECCPPFSFMTGAALSSQGTKPTTSHFSVLSFTPRQDHDITLCHVDESRKGVSAQRT 229
  ||:|||||
DB 142 -PELPKRS-----ISSNNSNVEDKDAV-AFTCEPEYDITYLWMINQSLPVPSP--- 189
  ||:|||||

QY 230 VRLRVAYAPRDL-VISISRNDTPDPENILRVNVSAQNR--VLENLGNSTSLPVL----- 282
  ||:|||||

```

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DB 190 -RLQLSNGNRITLTLSTVRNDTGPYCEIQNPVS-ANRSDPYTLNVTGPDITPISPSDT 247
QY 283 ----GQSICLVCTHSSPPARLSWTQRGVLSPSQSPDGVLEPRVOVEHGEFTCHAR 338
  ||:|||||
DB 248 YRRPGANLSTSCYAASNPPAQSWMILINGFOOSTOE-----LFIPIITVNNSGSYTCHAN 302
  ||:|||||
QY 339 H 339
DB 303 N 303

RESULT 10
5169835-17
; Patent No. 5169835
; APPLICANT: WAI-YEE, CHAN
; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,409
; FILING DATE: 07-AUG-1989
; SEQ ID NO:17:
; LENGTH: 321
5169835-17

Query Match      5.7%; Score 155; DB 6; Length 321;
Best Local Similarity 24.3%; Pred. No. 1.4e-05;
Matches 73; Conservative 43; Mismatches 105; Indels 80; Gaps 15;

QY 58 GY-WFKAVETTTKGAPVATNHSREVMSTRGRFOLGDPAGK-----NCSLYIRDAQ 109
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DB 64 GYSWYKG--ERYVDGNSLIVG-----VIGVQOATPGFANGSGRETIYFNASLLIONVT 113
  ||:|||||

QY 110 MDESQYFFERYKESYRYNFMNDGFLLKVTALTOKPDVYIPTLEPGQPVTVICVFNMA 169
  ||:|||||
DB 114 QNDTGFYTLQY-----IKSDLVNE-----EATGPFHY-----141
  ||:|||||

QY 170 FECCPPFSFMTGAALSSQGTKPTTSHFSVLSFTPRQDHDITLCHVDESRKGVSAQRT 229
  ||:|||||
DB 142 -PELPKRS-----ISSNNSNVEDKDAV-AFTCEPEYDITYLWMINQSLPVPSP--- 189
  ||:|||||

QY 230 VRLRVAYAPRDL-VISISRNDTPDPENILRVNVSAQNR--VLENLGNSTSLPVL----- 282
  ||:|||||
DB 190 -RLQLSNGNRITLTLSTVRNDTGPYCEIQNPVS-ANRSDPYTLNVTGPDITPISPSDT 247
  ||:|||||

QY 283 ----GQSICLVCTHSSPPARLSWTQRGVLSPSQSPDGVLEPRVOVEHGEFTCHAR 338
  ||:|||||
DB 248 YRRPGANLSTSCYAASNPPAQSWMILINGFOOSTOE-----LFIPIITVNNSGSYTCHAN 302
  ||:|||||
QY 339 H 339
DB 303 N 303

RESULT 11
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 05/5/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 416
; TYPE: prt
; ORGANISM: Bos Taurus

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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
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; PRIOR APPLICATION NUMBER: 60/090254
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; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          5.6%; Score 152.5; DB 4; Length 373;
Best Local Similarity 18.8%; Pred. No. 2.9e-05;
Matches 98; Conservative 69; Mismatches 182; Indels 173; Gaps 18;

QY      1 MLPLLLSSLLGSGAMDFWIRVOESVWVPEGLICISVPC--SFVSYPROD-----WTGS 53
DB      3 LLLLLLVSYVYVLTGLTTEIKRVAEEV-----TLRCHDGLGPEKDTIDEN--- 51
QY      54 TPAYGWKATVETTKAPVATNQSREV---EMSTRGRFOLTGDPAKNCISVIYRDAQ 109
DB      52 -----LITDNEGNQKVITYSSRHVYNNLTDEQKCHVAFASNFLAGDASIQTEPLK 102
QY      110 MODESQYFFRYER-GSYVRVNFNDGFELVLTALTOKPDVYIETLEPGQPVVICVFNW 168
DB      103 PSDEGRYCKYKNGRGRVWMSHVT-----LAVLPKSPKCELBELTEGSDTLTQCE--- 154
QY      169 AFEECPPPSPFSWGAALSSQGTKEFTTSHFSVLSFTPRPDHDTLTCNVDFSRKVSAGR 228
DB      155 -----SSSGTEPIYVYVWQ-----EKEGDERLP----- 167
QY      229 TVRLVAVYAPRDVLVISRNTPTDPPENLAVMSQANKRYLENLGNCTSLPYEGSLCL 288
DB      168 --RIR-----EKEGDERLP----- 180
QY      289 VCVTHSSPARLSMTQRGQVLSPOSPDPGLVLELPVROYEHEGEFTCHARHPLGSHVSL 348
DB      181 -----PKSRIDYNNHGRVLT-----LQNLIMSYSGLYCTAGNENAGKESCVV 221
QY      349 SLSVHKKGLISTAFNSGAFLLGITALFLCLALILMILPKRKRTOTETPRPRSRSNST 408
DB      222 RVTVOYVOSIGMVA--GAVTGIVAGALLIFLLVWLILIRKDKERYE--DEERPNFIREDA 277
QY      409 ILDIYVWPVTPAGLACRNOKATPNSPRPLPFGASPPSKKNOKQYOLDFPFPKSKST 468
DB      278 EAPKARLVKPPSSSSSSRSRSRSGSSSTRS-----TANSASRSOQTTLSTDAPOGLAT 330
QY      469 QA-----PESQESQ--ELHYATLNFPGVAPRPREARMKQTA 504
DB      331 QAYSIVGPVRSRSEPKVHHANLTKAETTP---SMIPSGSRA 369

RESULT 13
US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: TRYGVASON, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Leunkeri, Ulla
; APPLICANT: Mannikko, Minna
```



```

; TITLE OF INVENTION: Nephrlin Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,774
; FILING DATE: 18 MAR 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 97,842
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-040-774-2

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Query Match          5.6%; Score 151.5; DB 3; Length 1241;
Best Local Similarity 22.2%; Pred. No. 0.0002;
Matches 89; Conservative 55; Mismatches 146; Indels 111; Gaps 17;

QY 1 MLPLLLSLV--LGSQAMDGFRWIRNQSVMYPEGICISPCSFYPRQDMTSPAYG 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 LLLGLTLEGLAQALAIASVPRGW-ALPENLTVEGASVLEKCVSTP-----GSAV--- 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 59 YWFK-----AVYETTKGAPVATNHQSREVMSTRGRFQLTGDPKNCSLVIRDAQMODE 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 63 QMAKDGILLGPDRIPGFP-----RYRLEGDPARGEFHLHICADLSDD 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 114 SQFFVERGSGYRIRFMNDGFLKYTA-----LTQRPDYIIPTELRGQVYVYICVFNMA 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 107 AEVQCQYR-SEMGPELVSPRYLLSLVPPKLLLTPEAGTWTWVAGQEVVNCVSGDA 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 FECCPPPSFSGTGAALSSQGTKPTTSHFVLSFTPRPDHDTDLCHVD--FSKGVSAQ 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 166 -KAPDITLLSQOTIS-----DISAVNMGSSQOKLFYVE 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 228 RTVRLRVAYAPRDVLVISRDNTPDPPEMLRVVNSQANRTVLE-----NLGNGTSL 278
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 ATARV-----TPRSSDNQLLVCEASSPALEAPTKASFTVAVLPPPGP 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 279 PVLE-----GQSCLVGVTH--SSPPARLSMTQKQVSP-----SOPSDPGVL 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 PVLEWPGLEGHVRAQSLLEPCVARGGNPLATLQMLKNGQPVSTAMGTEHTQAVARSVL 302
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 321 ELPRVOVEHEGFEFTCHARHPL--GSOHVSLSLVHYKKGLI 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 VMTVREDHGAQLSCAHSNVSAGTQEHGTTLOVTPPPSAI 343

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RESULT 14
US-08-217-299-1
; Sequence 1, Application US/08217299
; Patent No. 5672513
; GENERAL INFORMATION:
; APPLICANT: Mach, J. P.
; APPLICANT: Pelegriin, A.

```

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; APPLICANT: Tersikh, A.
; TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,299
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93810214.2
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokras, Bruce A.
; REGISTRATION NUMBER: 32,748
; REFERENCE/DOCKET NUMBER: RAN 4093/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-5801
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 642 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-217-299-1

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Query Match          5.3%; Score 143; DB 1; Length 642;
Best Local Similarity 21.3%; Pred. No. 0.00043;
Matches 87; Conservative 53; Mismatches 143; Indels 126; Gaps 18;

QY 57 YGY-WFKAVYETTKGAPVATNHQSREVMSTRGRFQLTGDPKAG-----NCSLVIRDA 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 29 FGYSWYKG--ERVDG-----NRQIGVYITQCATPPGPAISGREIIPNMSLIGNI 78
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 109 QMODESOYFFRVERGSGYRIRFMNDGFLKYTA-----LTQRPDYIIPTELRGQVYVYICVFNMA 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 IQNDTGFYTLHVTKSLV--NEEATGQFR----- 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 AFECCPPPSFSGTGAALSSQGTKPTTSHFVLSFTPRPDHDTDLCHVDNFSKGVSAQR 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 106 VPELPPPS-----ISSNNSKPVEDKDAV-AFTCEPEQDATTYLMVWVNSQLPSP 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 229 TVRLRVAYAPRDVLVISRDNTPDPPEMLRVVNSQANRTVLE-----NLGNGTSL 281
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 156 --RLQLSNGNRRTLLFVNTVNDTASYKCEIQNVNARSRSVLTNLVLYGPDATPISPLNT 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 282 ----EGOSCLVGVTH--SSPPARLSMTQKQVSP-----SOPSDPGVL 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 214 SYRSGENLNLSCAHSNVSAGTQEHGTTLOVTPPPSAI 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 339 HPLGSOHVSLSLVHYKKGLISTAFSGNAPLIGITALLPLCLALLIMKILPRRRQGTET 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 269 NS-----DTGLNRTT-----VTI-----TYAEP 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 399 PRPRFSRHSF--ILDYINNVPTAGPLAOKR-----NOKATPNSPRTPL 439
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 20:02:07 : Search time 46 Seconds
(without alignments)
1793.429 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGSGQAMDGR.....RPEARPKGTQADVAEVKFO 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published.Applications-AA.*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2580.5	95.4	697	US-09-910-600-28	Sequence 28, App1
2	2576.5	95.2	697	US-09-984-130-149	Sequence 149, App
3	2278	83.7	544	US-09-910-600-8	Sequence 8, App11
4	2265	83.7	544	US-09-978-295A-259	Sequence 259, App
5	2265	83.7	544	US-09-978-697-259	Sequence 259, App
6	2265	83.7	544	US-09-978-192A-259	Sequence 259, App
7	2265	83.7	544	US-09-999-832A-259	Sequence 259, App
8	2265	83.7	544	US-09-978-189-259	Sequence 259, App
9	2265	83.7	544	US-09-978-608A-259	Sequence 259, App
10	2265	83.7	544	US-09-978-585A-259	Sequence 259, App
11	2265	83.7	544	US-09-978-191A-259	Sequence 259, App
12	2265	83.7	544	US-09-978-403A-259	Sequence 259, App
13	2265	83.7	544	US-09-978-564A-259	Sequence 259, App
14	2265	83.7	544	US-09-999-833A-259	Sequence 259, App
15	2265	83.7	544	US-09-981-915A-259	Sequence 259, App

16	2265	83.7	544	US-09-978-824-259	Sequence 259, App
17	2265	83.7	544	US-09-918-585A-259	Sequence 259, App
18	2265	83.7	544	US-09-978-423A-259	Sequence 259, App
19	2265	83.7	544	US-09-978-193A-259	Sequence 259, App
20	2265	83.7	544	US-09-999-830A-259	Sequence 259, App
21	2265	83.7	544	US-09-978-830A-259	Sequence 259, App
22	2265	83.7	544	US-09-978-187B-259	Sequence 259, App
23	2265	83.7	544	US-09-978-643A-259	Sequence 259, App
24	2265	83.7	544	US-09-978-375A-259	Sequence 259, App
25	2265	83.7	544	US-09-978-188A-259	Sequence 259, App
26	2265	83.7	544	US-09-978-296A-259	Sequence 259, App
27	2265	83.7	544	US-10-143-031A-259	Sequence 259, App
28	2265	83.7	544	US-10-002-967A-259	Sequence 259, App
29	2265	83.7	544	US-10-017-083A-259	Sequence 259, App
30	2265	83.7	544	US-10-143-030A-259	Sequence 259, App
31	2265	83.7	544	US-10-199-672-118	Sequence 118, App
32	2265	83.7	544	US-10-187-749-118	Sequence 118, App
33	2265	83.7	544	US-10-194-457-118	Sequence 118, App
34	2265	83.7	544	US-10-145-128A-259	Sequence 259, App
35	2265	83.7	544	US-10-184-642-118	Sequence 118, App
36	2265	83.7	544	US-10-196-747-118	Sequence 118, App
37	2265	83.7	544	US-10-173-688-118	Sequence 118, App
38	2265	83.7	544	US-10-173-690-118	Sequence 118, App
39	2265	83.7	544	US-10-173-691-118	Sequence 118, App
40	2265	83.7	544	US-10-173-692-118	Sequence 118, App
41	2265	83.7	544	US-10-173-694-118	Sequence 118, App
42	2265	83.7	544	US-10-173-698-118	Sequence 118, App
43	2265	83.7	544	US-10-173-707-118	Sequence 118, App
44	2265	83.7	544	US-10-174-569-118	Sequence 118, App
45	2265	83.7	544	US-10-174-569-118	Sequence 118, App

ALIGNMENTS

RESULT 1	US-09-910-600-28
Sequence 28, Application US/09910600	
Publication No. US20030036631A1	
GENERAL INFORMATION:	
APPLICANT: Longphre, Mallinda	
APPLICANT: Chang, Han	
APPLICANT: Whitney, Gena	
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF	
FILE REFERENCE: D0003NP	
CURRENT APPLICATION NUMBER: US/09/910.600	
CURRENT FILING DATE: 2001-07-20	
PRIOR APPLICATION NUMBER: 60/220.139	
PRIOR FILING DATE: 2000-07-21	
NUMBER OF SEQ ID NOS: 32	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 28	
LENGTH: 697	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Description of Artificial Sequence: L3-995-2	
US-09-910-600-28	
Query Match	95.4% Score 2580.5; DB 11; Length 697;
Best Local Similarity	73.2% Pred. No. 3.9e-195;
Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;	
QY	1 MLPLLLSLGSGQAMDGRFWRVQESVWVPPGLCISVPCSFYPRDWTGSTPAYGV 60
DB	1 MLPLLLSLGSGQAMDGRFWRVQESVWVPPGLCISVPCSFYPRDWTGSTPAYGV 60
QY	61 FKAVETTGAPATNHSREVMSTRGRFOLGDAKGCSTVIRDAQMDSSQYFFRY 120
DB	61 FKAVETTGAPATNHSREVMSTRGRFOLGDAKGCSTVIRDAQMDSSQYFFRY 120
QY	121 ERGSYRVNFMNDGFLLKVTALQKPDVYIPETLEFGQPVTVICVFNMAFECPSPFSFM 180

Db 121 ERGSYVRNENMDGFFLKAVTALNOKPDVYIPETLEPGQPVYICVFNMAFECCPPPSFW 180
QY 181 TGAALSSOGTKPTTSHTSFVSLFTPPRPODHDTLCHVDFSRKGSAGRTVRLVAAPRD 240
Db 181 TGAALSSOGTKPTTSHTSFVSLFTPPRPODHDTLCHVDFSRKGSAGRTVRLVAAPRD 240
QY 241 LVYSISDNTPD----- 252
Db 241 LVYSISDNTPALEPQGNVPLYEAQKGQFLRLCAADSPPATLSWLNQNRVLSSSH 300
QY 253 -----PENLRVWVSOANRTVLE 270
Db 301 WGRPRGLLELPVKAGDSGRYTCRAENRLGSGQALDLSVOYPPENLRVWVSOANRTVLE 360
QY 271 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVEHE 330
Db 361 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVEHE 420
QY 331 GEFTCHAHRLPGSOHVSLSLVHY----- 354
Db 421 GEFTCHAHRLPGSOHVSLSLVHYSPKLLGPSCSWEAEGLHCSSQASAPSLRWMLGE 480
QY 355 -----K 355
Db 481 ELLEGNSODSEFEVTPSSAGPMANSSLSLHGGLSGRLRCRAMVNHGAGSGSIILQLEPK 540
QY 356 KGLISTAFNSGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYIN 415
Db 541 KGLISTAFNSGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYIN 600
QY 416 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEKSSTOAPEQ 475
Db 601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEKSSTOAPEQ 660
QY 476 SOEELHYATLNFPGVRRPREARMKGTQADYAEVAKFO 512
Db 661 SOEELHYATLNFPGVRRPREARMKGTQADYAEVAKFO 697

RESULT 2

US-09-984-130-149
; Sequence 149, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PR489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-149

102(e)

Query Match 95.2%; Score 2576.5; DB 11; Length 697;
Best Local Similarity 73.0%; Pred. No. 8,2e-195;
Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
QY 1 MLPLILSLGSGQAMDGRFWLRVQSVWVPEGLCISVPCSFSTYPRQDWTGSTPAYGYW 60
|||||

Db 1 MLPLILSLGSGQAMDGRFWLRVQSVWVPEGLCISVPCSFSTYPRQDWTGSTPAYGYW 60
QY 61 FFAVETTKGAVATINHQSEVEMSTRGFFOLTGPANGNSLVTRDQMDDEQYFFRV 120
Db 61 FFAVETTKGAVATINHQSEVEMSTRGFFOLTGPANGNSLVTRDQMDDEQYFFRV 120
QY 121 ERGSYVRNENMDGFFLKAVTALNOKPDVYIPETLEPGQPVYICVFNMAFECCPPPSFW 180
Db 121 ERGSYVRNENMDGFFLKAVTALNOKPDVYIPETLEPGQPVYICVFNMAFECCPPPSFW 180
QY 181 TGAALSSOGTKPTTSHTSFVSLFTPPRPODHDTLCHVDFSRKGSAGRTVRLVAAPRD 240
Db 181 TGAALSSOGTKPTTSHTSFVSLFTPPRPODHDTLCHVDFSRKGSAGRTVRLVAAPRD 240
QY 241 LVYSISDNTPD----- 252
Db 241 LVYSISDNTPALEPQGNVPLYEAQKGQFLRLCAADSPPATLSWLNQNRVLSSSH 300
QY 253 -----PENLRVWVSOANRTVLE 270
Db 301 WGRPRGLLELPVKAGDSGRYTCRAENRLGSGQALDLSVOYPPENLRVWVSOANRTVLE 360
QY 271 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVEHE 330
Db 361 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVEHE 420
QY 331 GEFTCHAHRLPGSOHVSLSLVHY----- 354
Db 421 GEFTCHAHRLPGSOHVSLSLVHYSPKLLGPSCSWEAEGLHCSSQASAPSLRWMLGE 480
QY 355 -----K 355
Db 481 ELLEGNSODSEFEVTPSSAGPMANSSLSLHGGLSGRLRCRAMVNHGAGSGSIILQLEPK 540
QY 356 KGLISTAFNSGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYIN 415
Db 541 KGLISTAFNSGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYIN 600
QY 416 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEKSSTOAPEQ 475
Db 601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEKSSTOAPEQ 660
QY 476 SOEELHYATLNFPGVRRPREARMKGTQADYAEVAKFO 512
Db 661 SOEELHYATLNFPGVRRPREARMKGTQADYAEVAKFO 697

RESULT 3

US-09-910-600-8
; Sequence 8, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gene
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-600-8

Query Match 84.2%; Score 2278; DB 11; Length 544;
Best Local Similarity 75.1%; Pred. No. 2.1e-171;
Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;

PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598

PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

1 MLPLLLSLILGSGOAMGRFWIRVOESVWMPPEGICISVPCSFSPRODMGSPACGYW 60
1 MLPLLLSLILGSGOAMGRFWIRVOESVWMPPEGICISVPCSFSPRODMGSPACGYW 60
61 FKAVETTKGAPVATNHOSEVENSTGRFOLTDGPAGNCSLYIRDAOMODESOYFERY 120
61 FKAVETTKGAPVATNHOSEVENSTGRFOLTDGPAGNCSLYIRDAOMODESOYFERY 120
121 ERGSYVRNENMDGFEFLKYVTLTKPKDYVIEFTELEPGQPVVIVCFNMAFECCPPBSW 180
121 ERGSYVYVNFMDNDFELKVT----- 140
121 TGAALSOGTKPTSHFSVLSFTPPRODHDITLCHVDSKRGVSAORTVRLRAYAPRD 240
141 -----VLSFTPRPDHNDITLCHVDSKRGVSAORTVRLRAYAPRD 182
241 LVISISRDNTPD----- 252
183 LVISISRDNTPDLEPQGNVYLEAQGFRLILCAADSOBPATLSWLNRYLSSSH 242
253 -----PENLRVMYSQANRYVLE 270
243 WGPRLGLELPGVAKAGDSGRYTCRAENELGSGOALDLISVOY PENLRVMYSQANRYVLE 302
271 NLGNSTSLPYLEGOSLCVCTHSSPPARLSMTORGQVLSOPSODPVLELPRQVYHE 330
303 NLGNSTSLPYLEGOSLCVCTHSSPPARLSMTORGQVLSOPSODPVLELPRQVYHE 362
331 GEFTCHARHPLGSOHVSLSISVHYKKGLISTAFSNGAFUGITALLFLCALIIMKILP 390
363 GEFTCHARHPLGSOHVSLSISVHYKKGLISTAFSNGAFUGITALLFLCALIIMKILP 422
391 KRRTOTETPRPRFRSHSTIIDYINVPYAGGLAKRKNKATPNSRPTLPREGAPSPESK 450
423 KRRTOTETPRPRFRSHSTIIDYINVPYAGGLAKRKNKATPNSRPTLPREGAPSPESK 482
451 NOKKOYOLPSPPEKSSTOAPESQSOBELHYATLNFPGVPRPREARMKCTOADYAEVK 510
483 NOKKOYOLPSPPEKSSTOAPESQSOBELHYATLNFPGVPRPREARMKCTOADYAEVK 542

OY 511 FO 512
11
Db 543 FO 544

RESULT 5
US-09-978-697-259
Sequence 259, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/079664
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PRIOR APPLICATION NUMBER: 60/082700
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PRIOR FILING DATE: 1998-04-28

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PRIORITY APPLICATION NUMBER: 60/083392
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PRIORITY FILING DATE: 1998-04-29
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PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085579
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085573
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

Query Match      83.7%  Score 2265;  DB 10;  Length 544;
Best Local Similarity 74.8%  Pred. No. 2.3e-170;
Matches 450;  Conservative 1;  Mismatches 3;  Indels 148;  Gaps 2;

QY      1 MLPLLLSLLSGSGADGGRFWIVQSVWPEGLCTSVPCSESYPRQDWTGSTRPAQGYW 60
Db      1 MLPLLLSLLSGSGADGGRFWIVQSVWPEGLCTSVPCSESYPRQDWTGSTRPAQGYW 60

QY      61 FKAATETTKGAPVATINHQSEVENSTGRFQLTGDPKAGNCSTLVRDAOMODESQYFFRV 120
Db      61 FKAATETTKGAPVATINHQSEVENSTGRFQLTGDPKAGNCSTLVRDAOMODESQYFFRV 120
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Db      141 -----VLSFTPRPDHNTJLTVHDESRKGSVAORTVRLRVAYAPRD 182

QY      241 LVYSISRDNTPD----- 252
Db      183 LVYSISRDNTPALPEPQGNVYLEAKQGFRLLCADSDQPPATLSWLAQRVLSSSH 242

QY      253 -----PENLRNMSQAQRVYLE 270
Db      243 WCPRLGLELPEGVKAGDSGRYTCRAENRLSGQORALDLSVOYPPENLRNMSQAQRVYLE 302

QY      271 NLNGTSLPLVLEGSQSLCIVCVTHSSPPARLSWTORGQVLSPOSDPGVLELPRQVHE 330
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QY      331 GEFTCHARHPLGSGHVSLSLVYKKGILSTAFSNGARFLGIGITALLFLCLALITKILP 390
Db      363 GEFTCHARHPLGSGHVSLSLVYKKGILSTAFSNGARFLGIGITALLFLCLALITKILP 422

QY      391 KRRQTEPRPERSHSTILDYINVPYTAGPLAQRNOKATPNSPRTPLPGASPESEK 450
Db      423 KRRQTEPRPERSHSTILDYINVPYTAGPLAQRNOKATPNSPRTPLPGASPESEK 482

QY      451 NOKKOYOLPSEPEPKSSTQAPESQSEELHYATLNFPGVPRPEARMKGTQADYAEVK 510
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Db      543 FQ 544

RESULT 6
US-09-978-192A-259
Sequence 259, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gettisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630Pic9
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CURRENT APPLICATION NUMBER:	US/09/978,192A
PRIOR FILING DATE:	2001-10-15
PRIOR APPLICATION NUMBER:	09/918585
PRIOR FILING DATE:	2001-07-30
PRIOR APPLICATION NUMBER:	60/062250
PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/064249
PRIOR FILING DATE:	1997-11-03
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB 141 VLSISRDNTFALPPOQGNVPLYEAKOGFLLLCADSQPPTLSWVLONRVLSSSH 252
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DB 183 LVISISRDNTFALPPOQGNVPLYEAKOGFLLLCADSQPPTLSWVLONRVLSSSH 252
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DB 423 KRRTOTETPRPRSRHSTIIDYINVPTAGPLAQRKQKATPNSPRTPLPGAPSPSKK 482
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DB 483 NOKKOYOLPSPPEKSSTOAPESQSEELHYATLNPGVPRPREAPMPKGTQADYAEVK 542
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RESULT 7
US-09-999-832A-259

;; Sequence 259, Application US/09999832A
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;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
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;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C63
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53 PRIOR FILING DATE: 1998-05-15
54 PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7% Score 2265: DB 10: Length 544:
Best Local Similarity 74.8% Pred. No. 2.3e-170; Indels 148; Gaps 2;
Matches 450; Conservative 1; Mismatches 3;

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Db 363 GEFTCHARHPLGSOHSLSVHYKKGLISTAFSNGAFGIGTALLFCLAIITKILP 422
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Db 423 KRTOETPRPRSRSTIIDYINVVPTAGPLAQKNOKATPNSPTPLPGAPSPESK 482
QY 451 NOKKOYQLSPFPKKSSTOAPESQESQELHATLNFPGVRPPEARMKGTQADYAEVK 510
Db 483 NOKKOYQLSPFPKKSSTOAPESQESQELHATLNFPGVRPPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 8
US-09-978-189-259
Sequence 259, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fond, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978, 189
CURRENT FILING DATE: 2001-10-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2, 3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSSQAMDGRFWTRVQESVWVPEGLCTIVPCSFSPYRQDMTGSTPAYGYW 60
|||||
DB 1 MLPLLLSLGSSQAMDGRFWTRVQESVWVPEGLCTIVPCSFSPYRQDMTGSTPAYGYW 60
61 FKAFTETTKGAPATRNHQSREVEEMSTRGRFOLTGPDAKNCSLVIRDAQMODSQQYFFRV 120
|||||
DB 61 FKAFTETTKGAPATRNHQSREVEEMSTRGRFOLTGPDAKNCSLVIRDAQMODSQQYFFRV 120
121 ERGSYVRNPMNDGFLLKVTALTQKPDVYIPELPEQGPVTVICVENMAFEBCPPSFSW 180
|||||
DB 121 ERGSYVRNPMNDGFLLKVTALTQKPDVYIPELPEQGPVTVICVENMAFEBCPPSFSW 180
181 TGAALSSQGTKPTTSHFSVSTPRRODHTDLTCHVDPSRKGVSAORVRLVAYAPRD 240
|||||
DB 181 TGAALSSQGTKPTTSHFSVSTPRRODHTDLTCHVDPSRKGVSAORVRLVAYAPRD 240
141 -----VLSTPRQDHTDLTCHVDPSRKGVSAORVRLVAYAPRD 182
241 LVISISRDNTPD-----PPENLRVWVSQANRTYLE 270
|||||
DB 183 LVISISRDNTPDLEPQPGNVPLYLNAQKQFLRLCAADSQPPATLSWVLQNVLSSSH 242
253 -----PPENLRVWVSQANRTYLE 270
243 WGPRLPLGLEPGYKADSGRYTCTRAENRLGSOQRALDLSYQVPPENLRVWVSQANRTYLE 302
|||||
QY 271 NLGNSTSLPYLEQOSLCIVCTHSSPPARLSMTORGOVLSPPSPGVLELRVOYEH 330
|||||
DB 303 NLGNSTSLPYLEQOSLCIVCTHSSPPARLSMTORGOVLSPPSPGVLELRVOYEH 362
331 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 390
|||||
DB 363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 422
391 KRRTQETPRPRRSRSTIJDYINVPYTAGPLAQKRNQKTPMSPRTPLPGCAPSPESKK 450
|||||
DB 423 KRRTQETPRPRRSRSTIJDYINVPYTAGPLAQKRNQKTPMSPRTPLPGCAPSPESKK 482
451 NOKKQOLPSFPKPSSTOAPESQOSEELHYATLNPGRPRPEARMRGQADYAEVK 510
|||||
DB 483 NOKKQOLPSFPKPSSTOAPESQOSEELHYATLNPGRPRPEARMRGQADYAEVK 542
QY 511 FQ 512
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DB 543 FQ 544

RESULT 9
US-09-978-608A-259
; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC22
CURRENT APPLICATION NUMBER: US/09/978,608A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 259
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-608A-259

Query Match 83.7% Score 2265; DB 11; Length 544;
Best Local Similarity 74.8% Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSSLLGGSQAMDGREWIRVOESVWVPEGLCISVCSFSYPRQDWTGSTPAYGW 60
DB 1 MLPLLLSSLLGGSQAMDGREWIRVOESVWVPEGLCISVCSFSYPRQDWTGSTPAYGW 60
QY 61 FKAVETTTKGA PVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODSQYFFRV 120
DB 61 FKAVETTTKGA PVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODSQYFFRV 120
QY 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFMMAFECCPPPSFSW 180
DB 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFMMAFECCPPPSFSW 180
QY 181 TGAALSSGQKPTTSHSVLSFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRAYA PRD 240
DB 141 -----VLSFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRAYA PRD 182
QY 241 LVISISRDNDTPD-----PPENLRVWVSQANRTVLE 270
DB 183 LVISISRDNDTPALEPQGVNVPYLEAKGQFLKALCAADSQPATISWLNQNFVLSSSH 242
QY 253 -----PPENLRVWVSQANRTVLE 270
DB 243 WGPPELLELPYKAGDSGRYTCRAENRLSGQORALDLVQYPPENLRVWVSQANRTVLE 302
QY 271 NLNGTSLPYLESGSLCTVCTHSSPARLSWTQROGVSPSPSPGVLPRVOVEHE 330
DB 303 NLNGTSLPYLESGSLCTVCTHSSPARLSWTQROGVSPSPSPGVLPRVOVEHE 330
QY 331 GETTCARHP LGSQHSLSLSVHYKKGLISTAFSNGAFGIGTALLFTCLALLIMKTLIP 390
DB 363 GETTCARHP LGSQHSLSLSVHYKKGLISTAFSNGAFGIGTALLFTCLALLIMKTLIP 422
QY 391 KRTOETPRPRRSRSTILDYINVPYTAGPLAQKRNOKAMPNSPRTPLPGCAPSPESK 450

DB 423 KRTOETPRPRRSRSTILDYINVPYTAGPLAQKRNOKAMPNSPRTPLPGCAPSPESK 482
QY 451 NOKQYQLSFPPEPKSSITQAPESQSOEELHYATINFGVRRPEARMKGTQADYAEVK 510
DB 483 NOKQYQLSFPPEPKSSITQAPESQSOEELHYATINFGVRRPEARMKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 10
US-09-978-585A-259
Sequence 259, Application US/09978585A
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC15
CURRENT APPLICATION NUMBER: US/09/978,585A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 259
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
US-09-978-585A-259

Query Match 83.7% Score 2265; DB 11; Length 544;
Best Local Similarity 74.8% Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSSLLGGSQAMDGREWIRVOESVWVPEGLCISVCSFSYPRQDWTGSTPAYGW 60
DB 1 MLPLLLSSLLGGSQAMDGREWIRVOESVWVPEGLCISVCSFSYPRQDWTGSTPAYGW 60
QY 61 FKAVETTTKGA PVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODSQYFFRV 120
DB 61 FKAVETTTKGA PVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODSQYFFRV 120
QY 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFMMAFECCPPPSFSW 180
DB 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFMMAFECCPPPSFSW 180

QY 181 TGAALSSQGTTPPTSHFSVLSFTPRPDHDTDLTCHVDFSRKGVSAQRTVLRYAVAPRD 240
Db 141 -----VLSFTPRPDHDTDLTCHVDFSRKGVSAQRTVLRYAVAPRD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALEPOPOGNVYLAOKGQFLRLLCADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVYVSAQNTVLE 270
Db 243 WGRPRGLLEPGKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVYVSAQNTVLE 302
QY 271 NLNGSTSLPYLEQSLCLVCTHSSPPARLSMTORGQVLSPPSGVLELPRVQYEH 330
Db 303 NLNGSTSLPYLEQSLCLVCTHSSPPARLSMTORGQVLSPPSGVLELPRVQYEH 362
QY 331 GERTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFGLGITALFLCLALIKILP 390
Db 363 GERTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFGLGITALFLCLALIKILP 422
QY 391 KRRTQETPPRFRSRHSTIDYINVTAGPLAKRQKATPNSPRTPLPGAPSPESKK 450
Db 423 KRRTQETPPRFRSRHSTIDYINVTAGPLAKRQKATPNSPRTPLPGAPSPESKK 482
QY 451 NOKKQYQLBSPFPKSSSTQAPESQESQELHYATLNFPGVRRPPEARMPKGTQADYAEVK 510
Db 483 NOKKQYQLBSPFPKSSSTQAPESQESQELHYATLNFPGVRRPPEARMPKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 11

US-09-978-191A-259
Sequence 259, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978, 191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

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;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLSLLGSGQAMDGFRFMRVQESVWVPEGLCTSPGSESYPRQDWTGTPATGYW 60
|||
DB 1 MLPLLSLLGSGQAMDGFRFMRVQESVWVPEGLCTSPGSESYPRQDWTGTPATGYW 60
61 FKAVETTKGAPVATNMQSREVENSTRGRFQLTGDPKAGNCSLYTRDAQMDQESQYFRV 120
|||
DB 61 FKAVETTKGAPVATNMQSREVENSTRGRFQLTGDPKAGNCSLYTRDAQMDQESQYFRV 120
121 ERGSYVRNENNDGFEFLKVTALNOKPDVYIPELTIEPQPVYVICVFMAFECECPSEFSW 180
|||
DB 121 ERGSYVRNENNDGFEFLKVTALNOKPDVYIPELTIEPQPVYVICVFMAFECECPSEFSW 180
121 ERGSYVYNNFNDGFEFLKVTALNOKPDVYIPELTIEPQPVYVICVFMAFECECPSEFSW 140
|||
QY 181 TGAALSSQGTKPTTSHEFSVLSFTPRPODHTDLTCHVDFSRKGSQAORTVRLRVAYAPRD 240
|||
DB 141 -----VLSFTPRPODHTDLTCHVDFSRKGSQAORTVRLRVAYAPRD 182
241 LVISISRDNTPD----- 252
|||
DB 183 LVISISRDNTPALPOPOGNVPYLEAKQGFLLCAADSPPATLSWVLQNRVLSSHP 242
253 -----PPENLRVVSQANTVLE 270
|||
DB 243 WGPRLGLELPGYKAGDSGRYTCRAENRLGSGQRAIDLSVOYPPENLRVVSQANTVLE 302
271 NLNGSTSLPYLEQSLCLVCVTHSSPPARLSWTQRQVLSPPSQSDPGVLELPRVOEHE 330
|||
DB 303 NLNGSTSLPYLEQSLCLVCVTHSSPPARLSWTQRQVLSPPSQSDPGVLELPRVOEHE 362
331 GEFTCHARHPLGSOHSLSLSVHYKKGLISTAFSNGAFIGITALLFTCLALIMKILP 390
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DB 363 GEFTCHARHPLGSOHSLSLSVHYKKGLISTAFSNGAFIGITALLFTCLALIMKILP 422
391 KRRTQETPRPRFSRHSSTILDYINVPYTAGPLAOKNOKATPNSPTPLPAPAPSPESK 450
|||
DB 423 KRRTQETPRPRFSRHSSTILDYINVPYTAGPLAOKNOKATPNSPTPLPAPAPSPESK 482
451 NOKKOYOLSPFPKPSSTQAPESQSEELHATLNFPEVRRPRPEARMKGTQADYAEVK 510
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RESULT 12
US-09-978-403A-259
; Sequence 259, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIORITY APPLICATION NUMBER: 60/085580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085573
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

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Query Match 83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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1 MLPLLLSLGSGAANDGRFWITVQSVWVPEELCTISVCSFSPYPRQDWTGSTPAYGW 60
61 FKAUETTTGAPVATNHOSEVENSTGRFQLTGDPKAGKCSLYIRAOQODESOYFRV 120
61 FKAUETTTGAPVATNHOSEVENSTGRFQLTGDPKAGKCSLYIRAOQODESOYFRV 120
121 ERGIVRYNFMNDGFEFLKVALNOKPDVYIPELEPGQPVTVICVFNMAREECPSPFSW 180
121 ERGIVRYNFMNDGFEFLKVALNOKPDVYIPELEPGQPVTVICVFNMAREECPSPFSW 180
121 ERGIVRYNFMNDGFEFLKVALNOKPDVYIPELEPGQPVTVICVFNMAREECPSPFSW 180
121 ERGIVRYNFMNDGFEFLKVALNOKPDVYIPELEPGQPVTVICVFNMAREECPSPFSW 180
181 TGAALSSQGTTRPTSHSVEFTPRQDHTDILCHVDFSRKGYSAQRTVRLAVAYAPRD 240
181 TGAALSSQGTTRPTSHSVEFTPRQDHTDILCHVDFSRKGYSAQRTVRLAVAYAPRD 240
141 -----VLSFTPRQDHTDILCHVDFSRKGYSAQRTVRLAVAYAPRD 182
241 LVISISDNTPD----- 252
183 LVISISDNTPDALPEPOGNVPYLEAGKQGLALLCAADSQPATLISWLVQNRVLTSSSH 242

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QY 253 -----PENLRVMTSOANRYTLE 270
Db 243 WGPRLGLELPVKAKODSGRTYCRABENRLGSOQRALDLISVQYPPENLRVMTSOANRYTLE 302
QY 271 NIGNGTSLPVEEGSLCLVCYTHSSPPARLSWTORGQVLSPOSPDPGVELLPVQVEHE 330
Db 303 NIGNGTSLPVEEGSLCLVCYTHSSPPARLSWTORGQVLSPOSPDPGVELLPVQVEHE 362
QY 331 GEFTCHARRPLGSHVSTLSVHYKKGLISPAFSGARLGLIGITALLFLCLALITIMTLP 390
Db 363 GEFTCHARRPLGSHVSTLSVHYKKGLISPAFSGARLGLIGITALLFLCLALITIMTLP 422
QY 391 KRRTQETPRPRFSRHSHTILDYINVPYAGPLAQRNOKATPNSPRTPLPPGAPSPSK 450
Db 423 KRRTQETPRPRFSRHSHTILDYINVPYAGPLAQRNOKATPNSPRTPLPPGAPSPSK 482
QY 451 NOKKOYOLPSPPEKSSTOAPESSQSEELHYATLNFPGVPRPEARMKGTQADYAEVK 510
Db 483 NOKKOYOLPSPPEKSSTOAPESSQSEELHYATLNFPGVPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 13
US-09-978-564A-259
Sequence 259, Application US/09978564A
Publication No. US20030050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978, 564A
CURRENT FILING DATE: 2001-10-16
PRIORITY APPLICATION NUMBER: 09/918585
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/064249
PRIORITY FILING DATE: 1997-11-03
PRIORITY APPLICATION NUMBER: 60/065311
PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066364
PRIORITY FILING DATE: 1997-11-21

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[illegible]

; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 11; Length 544;
 Best Local Similarity 74.8%; Pred. No. 2,3e-170;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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QY 1 MLPLLSLILGSGAMDRFWIRVOESVMEPEGICISVPSSEFSPRODMGSTRPAGW 60
DB 1 MLPLLSLILGSGAMDRFWIRVOESVMEPEGICISVPSSEFSPRODMGSTRPAGW 60
QY 61 FRAVETTKGAPVATNHOSREVEEMSTRGRFOLTPDPAKNGSLVIRDAQMODESQFFRV 120
DB 61 FRAVETTKGAPVATNHOSREVEEMSTRGRFOLTPDPAKNGSLVIRDAQMODESQFFRV 120
QY 121 ERGSVYRNFENMDGFLVLTALTKRDVYIIPETLEPGQPVYICVFNNAFEECPPEFSW 180
DB 121 ERGSVYRNFENMDGFLVLTALTKRDVYIIPETLEPGQPVYICVFNNAFEECPPEFSW 180
QY 181 TGAALSSOGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGSAGQRTVRLRVAYARD 240
DB 181 TGAALSSOGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGSAGQRTVRLRVAYARD 240
QY 141 -----VLSETPRPQDHNDLTCVHDFSRKGSAGQRTVRLRVAYARD 182
DB 141 -----VLSETPRPQDHNDLTCVHDFSRKGSAGQRTVRLRVAYARD 182
QY 241 LVISIRNDTP----- 252
DB 241 LVISIRNDTP----- 252
QY 183 LVISIRNDTPALPEPQGNVYLEAKGQELRLCAADSOPTATLSWLNRYLSSHP 242
DB 183 LVISIRNDTPALPEPQGNVYLEAKGQELRLCAADSOPTATLSWLNRYLSSHP 242
QY 253 -----PENLRYVMVSQANRYTLE 270
DB 253 -----PENLRYVMVSQANRYTLE 270
QY 243 WGPRLGLELPGVAKGDSGRYTCRAENRLGSOQRALDISVQYPPENLRYVMVSQANRYTLE 302
DB 243 WGPRLGLELPGVAKGDSGRYTCRAENRLGSOQRALDISVQYPPENLRYVMVSQANRYTLE 302
QY 271 NLGNGSTLPVLEGGSLCIVTTHSSPPARLSWTOGVOVLSPOSDPGLBLPRVOYEH 330
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QY 303 NLGNGSTLPVLEGGSLCIVTTHSSPPARLSWTOGVOVLSPOSDPGLBLPRVOYEH 362
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QY 331 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFLGIGITALLFLCLALITIMILP 390
DB 331 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFLGIGITALLFLCLALITIMILP 390
QY 363 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFLGIGITALLFLCLALITIMILP 422
DB 363 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFLGIGITALLFLCLALITIMILP 422
QY 391 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 450
DB 391 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 450
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RESULT 14
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 ; Publication No. US20030054405A1
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 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Gao, Wei-Qiang

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; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjaevlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999, 833A
; CURRENT FILING DATE: 2001-10-24
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Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2

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OY      61 FKAVETTTKGAPVATNHOSREVENSTRGRFOLTGDPAKNCSLVTRDAOMODESOFYFRV 120
DB      61 FKAIVETTTKGAPVATNHOSSREVEMSTRGRFOLTDGPAGKNCSLVTRDAOMODESQYFFRV 120
OY      121 ERGSVVRKNENMDGFELKVTAALTKQRPDIYEITLEPGQPVIYICFNMAFEBCPPPSFW 180
DB      121 ERGSVVTYNFNMDGEFLKYT----- 140
OY      181 TGAALSOGTPTTSHFSVLSTFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLVAAYARD 240
DB      183 LVISTSRDNTALEPOPOGNPYILEAKOCOPFLRLCAADSOPTATLAWLONRVLSSHP 242
OY      241 LVISTSRDNPD----- 252
DB      253 ----- 270
OY      243 WGPRLPLGLELPGVAKAGDSGRITTCRAENRLGSQQRALDLISVOYTPENLRMYMSQAARTYLE 302
DB      271 NLNGNTSLPVLEGOSLCVCTVTHSSPPARLSWTORGVALSPSQSDPGVLELPRVOVEHE 330

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 QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFGIGTALLFLCLALIIKKIIP 390
 Db 363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFGIGTALLFLCLALIIKKIIP 422
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 / APPLICANT: Bolstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerder, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Guiney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kijavlin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Shelton, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
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Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB      61 FKAVETTKGAPVATNHQSEVEMSTRGRFQLTGPAPKNCSLVIRDAQMOQESQYFFRV 120
QY      121 ERGSYVRNFMNDGFFLKATLTQKPDVYIPELTBGCQVYVICVFNMAFECCPPPSFW 180
DB      121 ERGSYVYTNFMNDGFFLKVT----- 140
QY      181 TGAALSSQGTKPTTSHFSVLTPTPRPDHDTDLTCHVDSRKGVSAORTVRLRVAYAPRD 240
DB      141 -----VLSFTPRPDHNTDLTCHVDSRKGVSAQRTVRLRVAYAPRD 182
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DB      183 LVYSISRDNTPALPEPQGNVPLYLEAQKQFLRLLCADSQPPATLSWVLQNRVLSSHP 242
QY      253 -----PPENLRVMSQANFTVLE 270
DB      243 MGPRPLGLELPGVKAAGDSGRYTCRAENRLSGOORALDLSVQYPPENLRVMSQANFTVLE 302
QY      271 NLGNGTSLPYLEGOSLCTVCVTHSSPPARLSWTORGQVLSPOSPDPGLLELPRVOVEH 330
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QY      331 GEFTCHARPPLGSOHVSLSLSVHYKKGLISTAFNSGAFIGITALLLFLCLALLIMKILP 390
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:03:42 : Search time 5699 Seconds -
(without alignments)
3675.334 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2580.5	95.4	2208	6 AX365530	AX365530 Sequence
3	2580.5	95.4	3012	9 AF301007	AF301007 Homo sapi
4	2580.5	95.4	3024	6 AX365542	AX365542 Sequence
5	2576.5	95.2	2176	9 AF310233	AF310233 Homo sapi
6	2278	84.2	2565	6 AX365516	AX365516 Sequence
7	2265	83.7	2764	6 AX376050	AX376050 Sequence
8	2220.5	82.1	3099	6 BD011516	BD011516 Sequence
9	2220.5	82.1	3099	6 BD011517	BD011517 Sequence
10	2196.5	81.2	2126	6 AY032685	AY032685 Homo sapi
11	2142.5	79.2	2294	6 AX365517	AX365517 Sequence
12	1960	72.4	2321	6 AX497858	AX497858 Sequence
13	1929.5	71.3	2823	6 AX365518	AX365518 Sequence
14	1824	67.4	2529	6 AX365544	AX365544 Sequence
15	1728	62.1	1665	6 AX365519	AX365519 Sequence
16	1680.5	62.1	2154	6 AX430336	AX430336 Sequence
17	1665.5	61.6	8400	9 AY029277	AY029277 Homo sapi
18	1666.5	61.6	143045	9 AC008750	AC008750 Homo sapi
19	1646.5	60.8	195993	2 AC134953	AC134953 Homo sapi
20	1513.5	55.9	3183	9 AF337818	AF337818 Homo sapi
21	1503.5	55.6	2273	9 AB072038	AB072038 Homo sapi
22	1454.5	53.8	2052	6 AX365546	AX365546 Sequence
23	1389.5	51.3	2605	6 BC039008	BC039008 Homo sapi
24	1366	50.5	17216	2 AC130272	AC130272 Homo sapi
25	1343.5	49.6	2067	10 AY210400	AY210400 Mus muscu
26	1337	49.4	167266	2 AC130273	AC130273 Homo sapi
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28	1160.5	42.9	146741	9 AC011452	AC011452 Homo sapi
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36	909	33.6	2180	9 BC035809	BC035809 Homo sapi
37	900	33.3	1554	6 AX365520	AX365520 Sequence
38	896.5	33.1	2930	9 AF195092	AF195092 Homo sapi
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS Li, N., Zhang, W., Wan, T., Zhang, J., Chen, T., Yu, Y., Wang, J. and
 Cao, X.
 TITLE Cloning and characterization of siglec-10, a novel sialic acid
 binding member of the Ig superfamily, from human dendritic cells
 JOURNAL J. Biol. Chem. 276 (30), 28106-28112 (2001)
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 PUBMED 11359381
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 2 (bases 1 to 3124)
 AUTHORS Li, N., Zhang, W., Wan, T. and Cao, X.
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 JOURNAL Submitted (15-AUG-2001) Department of Immunology, Second Military
 Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China
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 Db 403 TTCAAGACGAGTACGACGACACACACAGGGTGTCTGTGGCCACCAACACAGAGTGA 462
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 QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
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 QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuIysValThr 140
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 QY 141 AlaLeuThrGlnLysProAspValTyrTleProGluThrLeuGluProGlyGlnProVal 160
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 QY 161 ThrValIleCysValAlaPheAsnThrAlaPheGlnGluCysProProSerPheSerTrp 180
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 QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrIysProThrThrSerHisPheSerValLeu 200
 Db 763 ACGGGGGCTGCCCTCTCTCCCAAGAACCAACCAACAGCTCCCACTTCACTGCTC 822
 QY 201 SerPheThrProAlaGlyProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
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 QY 221 ArgIysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
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 QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp 252
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 QY 252 252
 Db 1003 GTCCCAATACCTGGAAGCCCAAAAGGCCAGTTCTCGGGCTCTGTGCTGACAGC 1062
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QY	331	GLYGLUPHETHRYSHLSALARGHISProleuLyserglnHISvalSerLeuSerLeu	350
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QY	351	SerValHISryrLysGLyleuLISerThrAlaPheSerAsnGLyAlaPheLeuGLy	370
Db	1543	TCCGTGCACrTAAAGMAGGACrTATCTCAACGGCATTCTCCAAACCGAGCCTTCTGGGA	1602
QY	371	ILleGLyILeThrAlaLeuLeuPheLeuLysLeuAlaLeuILeILeMetLysILeLeuPro	390
Db	1603	ATCGGCArTACAGGCTCTTCTTCTCTGCTGCTGGCCCGATCArTCAAGAATTCrTACCG	1662
QY	391	LysArGArThrGLInThrGLuThrProArGProArPheSerArGHISSerThrILeLeu	410
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QY	411	AspYrILeAsnValILeProThrAlaGLyProLeuAlaGLInLysArGAsnGLInLysAla	430
Db	1723	GATrTACArTCAArTGGrTCTCCGACGCGTGGCCCTGCTGCAGAAACCGAArTCAAAAGCC	1782
QY	431	ThrProAsnSerProArGThrPhIProLeuProGLyAlaProSerProGLuSerLysLys	450
Db	1783	ACACCAAAACArTCTCGGACCCCTrTTCACAGAGTGTCTCCrTCCCAAGATCAAAAGAG	1842
QY	451	AsnGLInLysLysGLInYrGLInLeuProSerPheProGLuProLysSerSerThrGLInAla	470
Db	1843	AACCAAGAAAAGCAGrTATCAGrTTCGCCAGAGrTTCACCAAArTATCATCATCAAGACC	1902
QY	471	ProGLuSerGLInLysergInGLuGLInLeuHISryrAlaThrILeAsnPheProGLyAla	490
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QY	491	ArGProArPProGLuAlaArGMeProLysGLInThrGLInAlaAspYrAlaGLuValLys	510
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Db	2023	TTCCAA 2028	
RESULT 2			
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DEFINITION	Sequence 15 from Patent WO0208257.		
VERSION	AX365530		
ACCESSION	AX365530.1	GI:18697092	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 Longphre,M., Chang,H. and Whitney,G.		
JOURNAL	Novel singlecs and uses thereof		
FEATURES	Patent: WO 0208257-A 15 31-JAN-2002;		
SOURCE	BRISTOL-MYERS SQUIBB COMPANY (US)		
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ORIGIN			
Alignment Scores:			
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Score:	2580.50	Matches:	510
Percent Similarity:	73.31%	Conservative:	1
Best Local Similarity:	73.17%	Mismatches:	1
Query Match:	95.36%	Indels:	185
Db:	6	Gaps:	2

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Db	118	ATGCTACTGCGACAGCTGCTGTCTCCCTGCTGGGGGGGCTCCAGGCTATGATGGAGAGA	177
OY	21	PheTrpIleArgValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro	40
Db	178	TTCTGGATACAGAGTGCAGAGTCAAGTATGGTGGCGAGAGGGCCGTGCATCTCTGTGCC	237
OY	41	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	238	TGCTCTTTCCTCTACACCCCGACAGACAGTGCAGAGGCTCTACCCACGTTATAGCTACTGG	297
OY	61	PheIysAlaValIleThrGluThrThrThyGlyAlaProValAlaIleTrpAsnHisGlnSerArg	80
Db	298	TTCAAGCAGTACTAGACACACCAAGGGTCTCTGTGGCCACCAACACACAGTGTGA	357
OY	81	GluValGlnMetSerThrArgIleArgPheGlnLeuThrGlyAspProAlaIysGlyAsn	100
Db	358	GAGGTGAATAATGAGACACCCGGGGCGGATTTCCAGTCACTGGGGGATCCCGCCAAAGGGAAC	417
OY	101	CysSerLeuValIleIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	120
Db	418	TGCTCCCTGGTGATCAGAGAGCGCCAGTGTGAGGATGTGATCAGCTACTCTTCTTGGGTG	477
OY	121	GluTrpArgIleSerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuIysValThr	140
Db	478	GAGAGAGAACACTATGTACATATATATTTCAATGAACGATGGGCTTCTTTAAAGTAAACA	537
OY	141	AlaLeuThrGlnIlyProAspValTyrIleProGluThrLeuGluProGlyGlnProVal	160
Db	538	GCCCTGATCTCAGAAAGCTGATGTACTATCCCGGAGACCTGTGGAGCCGGGACCGGGTG	597
OY	161	ThrValIleCysValAlaPheAsnTrpAlaPheGlnGluCysProProPheSerPheSerTrp	180
Db	598	ACGGTCATCTGTGTGTTTAACGTGGGCCTTTAAAGAAATCCACCCCTTCTTCTCTCGG	657
OY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrIlyProThrTrpSerHisPheSerValLeu	200
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Db	718	AGCTTACGGCCCGACCCCGAGGACCCACACACCGGACTCACCCTGGCAATGTGACTTCTCC	777
OY	221	ArgIlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrValProArgAsp	240
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Db	898	GTCCCATACCTGGAGAGCCCAAAAGGCCAGTTCTTCGGGGCTCTCTGTGTGCTGACAGC	957
OY	252	-----	252
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OY	252	-----	252
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OY	253	-----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	270
Db	1138	CAGTATCCTCCAGAGAACCTGATGATGTGTTTCTCCCAAGCAACAGCAGCATGCTCTGTGA	1197

OY		271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlnSerLeuCysLeuValCys	290
Db		1198	AACCTTGGGAAGCGCACGTCTCTCCAGTAATGGAGGACCAAAACCTGTGCCTGTGT	1257
OY		291	ValThrHisSerSerProProlAArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	310
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OY		311	ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnHisGlu	330
Db		1318	CCCACCACAGCCCTCAGACCCCGGGGCTCTTGAGCTGTGCTCGGATTCAAAGTAGACACGAAA	1377
OY		331	GlyGlnPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db		1378	GGAGAAGTTCACTCTCCACGACGCTGGCACCCACTGGGGCTCCACGACGTCCTCTCAGCCTC	1437
OY		351	SerValHisIleTyrr-----	354
Db		1438	TCCGTGCACACTCTCCCGAAGCTGTGGGCCCTTCCTGTCTCTGGAGAGCTGAGAGGCTGTG	1497
OY		354	-----	354
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OY		354	-----	354
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OY		354	-----	354
Db		1618	CCCTGGGCGAACAAGCTCCCTCTGAGCCTCATGAGAGGCTCAGCTCCGGGCTTCAGGCTCCGC	1677
OY		355	-----Lys	355
Db		1678	TGTGAGGCGCTGGAACGTCAATGGGGCCACAGTGGATCCATCTCGACAGCTCCAGATTAAG	1737
OY		356	LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla	375
Db		1738	AAGGACACATCTCAACCGGCAATCTTCCAAACGAGCAGCTTCTGGGGAATCGGATCAACGGCT	1797
OY		376	LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGln	395
Db		1798	CTTCTTTTCTCTGCTGCTGGCCCTGATCTCATCTGAAGATTCTACCGAAGACAGCACTCAG	1857
OY		396	ThrGlnThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal	415
Db		1858	ACAGAAACCCCGAGGCCCCAGGTCTTCCCGCAGACAGCAATCTGGATTACATCAATAAGTG	1917
OY		416	ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro	435
Db		1918	GTCCCGAGGCTGGGCCCTCTGGCTCAGAAAGCGAATCGAAGAACCCACCAACAGTCTCT	1977
OY		436	ArgThrProLeuProProGlyAlaProSerProGlnSerLysLysAsnGlnLysGln	455
Db		1978	CGAACCCTCTTCCACCAAGGTGCTCCCTCCACAGATCAAGAAAGAACCAAAAAAGAG	2037
OY		456	TyrlGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGlnSerGlnGlu	475
Db		2038	TATCAGTTGCCACAGTTTCCAGAAACCCAATCATCTCACTCAAGGCCCAAGAAATCCAGAG	2097
OY		476	SerGlnGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlyValAlaGProArgProGlu	495
Db		2098	AGCCCAAGAGAGCTCCATTATGCCAGCTCAACTTCCAGGCGTCAAGACCCAGGCGCTGAG	2157
OY		496	AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLysPheGln	512
Db		2158	GCCCGGAGTCCCAAGGCGCACCCAGCGGATTTATGACAGAAAGTCAAGTTCCAA	2208
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LOCUS			Homo sapiens stialic acid-binding immunoglobulin-like lectin 10	
DEFINITION			(STGBL10) mRNA, complete cds.	

Accession	AF301007.1	GI:21956185
KEYWORDS	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Mumukshu, Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteleostomi; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	Whitney, G.S., Wang, S., Chang, H., Cheng, K.-Y., Liu, P., Zhou, X.D., Yan, W.P., and Longpre, M.	
TITLE	A new Siglec family member, SIGLEC10, is expressed in cells of the immune system and has signaling properties similar to CD33	
JOURNAL	J. Biol. Chem. 275(1):1-10 (2000)	
AUTHORS	Longpre, M., Whitney, G.S., Wang, S., Chang, H., and Yan, W.P.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-AUG-2000) Immunology Department, Bristol-Myers Squibb Pharmaceutical Research Institute, Route 206 and Province Line Road, Princeton, NJ 08543-4000, USA	
FEATURES	<p>Location/Qualifiers</p> <p>1..3012</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/chromosome="19"</p> <p>/map="19q13.33-q13.41"</p> <p>1..3012</p> <p>/gene="SIGLEC10"</p> <p>118..2211</p> <p>/gene="SIGLEC10"</p> <p>/codon_start=1</p> <p>/product="sialic acid-binding immunoglobulin-like lectin 10"</p> <p>/protein_id="AA083254.1"</p> <p>/db_xref="GI:21956186"</p> <p>/translation="MLPLILSLISLGGSGAMDGRFWRVQESVAVPEGLCISVPCSS YPRDWDGSPAYGMYKFAVETKTKGAPVATNHSREVSSTGRDITDPAKGNCS LVTIDQADQDSQIFFRYERKSGYRINRNMNDGLTKATLQKRDYITPETLEGGQV TVTCVFMWAFEECPSPFSWGAALSSQGRKPTVSHSVLSFTPRPDNHTDLCHVD FSRGVSAGORTVRLRVAVAPRDVLSISRNTPALPEQGVNVPYLEAKNGQPLRLC AADQSPATLSWLVQNRVLSSSHWPGRPLGLEPGVAKDSDGYTCRAKNGLSQOR ALDLSVQPEPNTLVMVSOAKRVYLENGTSLPVEGSLCLVCTHSSPPRLSM TORQVLSQSPDPGVLEPRVQVEHGEGETCARPLDSOHVLSLSVYSPKLLG PSCGWEAEGELSCSSQASAPASLRMLGLGELLGNSDQSPFETPSAAPMNSLS LHGSLSSGLRLRCANVHCAOSSITQLDPKKLISITAFSNAPGLCITALLFCLT ALIIMLKLPKRTTETPRPFSKSHSTLLDITNVYPAIGLQKRNKATPNSERTPL PPGASPESSKKNQKQYOLBPFEPKSSQAPESQESQELHVAITLNFPPVPRPEAR MKQGTQADYAEVKKIO"</p>	
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QY	21 PheTrpIleArgValGlnGlnSerValMetValProGluGlyLeuGlyIleSerValPro	40
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Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
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Qy 355 -----Lys 355
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RESULT 4
AX365542
LOCUS AX365542 3024 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 27 from Patent WO0208257.
ACCESSION AX365542
VERSION AX365542.1 GI:18697098
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Longphre, M., Chang, H. and Whitney, G.
TITLE Novel siglecs and uses thereof
JOURNAL Patent: WO 0208257-A 27 31-JAN-2002;
BRIEF-ABSTRACT BRISTOL-MYERS SQUIBB COMPANY (US)
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Qy	496	AlaHrwtProlYsgLYThrGlnAlaAspTYrAlaGluValIysPheGln	512
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AF310233			
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TITLE			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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Pred. NO.:			
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Q	291	ValIhrHisSerSerProProAlaIArgLeuSerThrIhrGlnIArgGlyGlnValLeuSer	310
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DEFINITION	Sequence 1 from Patent WO0208257.				
ACCESSION	AX365516				
VERSION	AX365516.1	GI:18697085			
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SOURCE					
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AUTHORS	1 Longphre,M., Chang,H. and Whitney,G.				
TITLE	Novel siglecs and uses thereof				
JOURNAL	Patent: WO 0208257-A 1 31-JAN-2002;				
	BRISTOL-MYERS SQUIBB COMPANY (US)				
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RESULT 7
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LOCUS AX376050
DEFINITION Sequence 117 from Patent WO0168848.
ACCESSION AX376050
VERSION AX376050.1 GI:19170417
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
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Genentech, Inc. (US)
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AUTHORS Kikly,K.K. and Miller,C.L.E.
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Qy 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
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Qy 252 ----- 252
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Qy 253 -----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
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Qy 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 290
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LOCUS S140adhesin family 4(SAF-4) cDNA.
DEFINITION BD011517
ACCESSION BD011517.1 GI:18639890
VERSION JP 2001502359-A/2.
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 3099)
AUTHORS	Kikly,K.R. and Miller,C.L.E.
TITLE	Sialodhesin family 4(SAF-4) cDNA
JOURNAL	Patent: JP 2001502359-A 2 20-FEB-2001; SMITHKLINE BEECHAM CORP
COMMENT	OS Homo sapiens (human) PN JP 2001502359-A/2 PD 20-FEB-2001 PE 27-MAY-1998 JP 1999500864 PR 27-MAY-1997 US 60/047572 PI KRISTINE KAY KIKLY,CONNIE LYNN ERICKSON MILLER PC A61K33/00,A61K39/335,A61K48/00,C07H21/04,C07K14/435,C07K14/705, PC C07K16/00, PC C07K16/18,C07K16/28,C12N15/01,C12N15/11,C12N15/12,C12N15/63 CC
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 DEFINITION Sequence 2 from Patent WO0208257.
 ACCESSION AX365517
 VERSION AX365517.1 GI:18697086
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 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Longpre, M., Chang, H. and Whitney, G.
 TITLE Novel siRNAs and uses thereof
 JOURNAL Patent: WO 0208257-A 2 31-JAN-2002; BRISTOL-MYERS SQUIBB COMPANY (US)
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VERSION      AX497858.1 GI:23342965
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ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Baughn, M.R., Lu, D.A., Yue, H., Elliott, V.S., Thanagavelu, K., Ramkumar, J., Lu, Y., Lo, T.P., Gururajan, R., Gandhi, A.R., Arvizu, C. and Yao, M.G.
TITLE      Immunoglobulin superfamily proteins
JOURNAL      Patent: WO 0240671-A 8 23-MAY-2002;
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ORIGIN

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QY 106 ArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgValGluArgGlySerTyr 125
DB 182 AGACAGCCGACATGACGATGATGACAGTACTTCTTTCGGGTGAGAGAGAGAGTAT 241
QY 126 ValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLys 145
DB 242 GTGAGATATATTTATGAAAGATGGGTTCTTTAAAGTAAACACCCCTGACTGAAAG 301
QY 146 ProAspValTyrIleProGlnThrLeuGlnProGlyGlnProValThrValIleCysVal 165
DB 302 CCGTGTGTCTACATCCCGACAGACCTGGAGCCGGGACCGGTGACGGTCACTCTGTG 361
QY 166 PheAsnTrpAlaPheGlnGluCysProProSerPheSerTrpThrGlyAlaAlaLeu 185
DB 362 TTTAACTGGGCTTTGAGGAATGTCACCCCTCTTCTCTCGAGCGGGGCTGCGCTC 421
QY 186 SerSerGlnGlyThrLysBroThrThrSerHisPheSerValLeuSerPheThrProArg 205
DB 422 TCCTCCCAAGAAACCAACCAAGCACTCCACTCTCTCACTGCTGACGCCACAG 481
QY 206 ProGlnAspHisAspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSer 225
DB 482 CCCAGGAGCACAAACACGACCTCACTCCATGTGACTCTCCAGAAAGGCTGAGC 541
QY 226 AlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIle 245
DB 542 GTACAGAGAGACCGTCCGACTCCGTGTGGCTATGCCCCCAGAGACTTGTATCAGCAT 601
QY 246 SerArgAspAsnThrProAsp----- 252
DB 602 TCACGTGACAAACACGACGACCTCGAGCCCAAGCCCAAGGAAATGTCCCATACGTGA 661
QY 252 ----- 252
DB 662 GCCCAAAAAGCCAGTTCTCTGGGCTCTCTGTGCTGTGACAGCCAGCCCTGACACA 721
QY 252 ----- 252
DB 722 CTGAGCTGGGTCTCTGACAGACAGAGTCTCTCTCTGCCATCCCTGGGGCCCTAGACC 781
QY 252 ----- 252
DB 782 CTGGGCTGGAGCTGCCGGGGTGAAGGCTGGGGATTGAGGGGCTACACCTGGCAGAG 841
QY 253 -----ProGlu 255
DB 842 GAGAACAGGCTTGGCTCCAGCAGGAGCCCTGAGCTCTCTGTGCAGTATCCTCCAGAG 901

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QY 256 AsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlnAsnLeuGlyAsnGly 275
DB 902 AACCTGAGAGTGAFTGGTTTCCCAAGCAACAGGACAGTCTCGAAAACCTGGGAACGGC 961
QY 276 ThrSerLeuProValLeuGlnGlyGlnSerLeuCysValThrHisSerSer 295
DB 962 AGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTGTCTCAACACAGCAGC 1021
QY 296 ProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSer 315
DB 1022 CCCCCAGCCAGGCTGAGCTGAGACCCAGAGGGGACAGTTCTGAGCCCTCCAGCCCTCA 1081
QY 316 AspProGlyValLeuGlnLeuProArgValGlnValGlnHisGlnGlyGlnPheThrCys 335
DB 1082 GACCCGGGGTCTCGAGGCTGCTCGGGTTCAAGTGAGACAGAGAGAGTTCACCTGC 1141
QY 336 HisAlaArgHisProLeuGlnSerGlnHisValSerLeuSerLeuSerValHisTyrLys 355
DB 1142 CACGCTCGGACACCACTGGGCTCCAGCAGCTCTCTCAGCCTCCGTCGACTATTAAG 1201
QY 356 LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla 375
DB 1202 AAGGACTCATTCACAGGCAATTCACCAAGGAGCGTTCTGGAAATCGGCATCAGCGCT 1261
QY 376 LeuLeuPheLeuCysLeuAlaLeuIleIle 385
DB 1262 CTTCTTTCTCTGCTGCGCTGAGCTGATCATG 1291

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Search completed: October 8, 2003, 21:48:29
Job time : 5749 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:03:17 ; Search time 408 Seconds
(without alignments)
3387.530 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
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Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2706	100.0	1536	21	AAA37847	Human obesity prot
2	2580.5	95.4	2208	24	ABK43367	DNA encoding stail
3	2580.5	95.4	3024	24	ABK43373	DNA encoding stail
4	2278	84.2	2565	24	ABK43360	DNA encoding stail
5	2265	83.7	2764	20	AAZ34109	Human PRO340 nucle
6	2265	83.7	2764	21	AACT8510	Human PRO340 (UNQ4
7	2265	83.7	2764	22	AAAS5983	Human DNA encoding
8	2265	83.7	2764	25	ACAS7741	Human PRO940 cDNA.
9	2265	83.7	2764	25	ABX98211	Human cDNA encodin
10	2265	83.7	2764	25	ABX98713	Novel human secret
11	2265	83.7	2764	25	ACA05758	Human secreted/tri
12	2265	83.7	2764	25	ABX92481	cDNA encoding huma
13	2265	83.7	2764	25	ABX97802	Human PRO polynuc
14	2265	83.7	2764	25	ABX78586	Human PRO polynuc
15	2265	83.7	2764	25	ABX75599	Human cDNA encodin
16	2265	83.7	2764	25	ABX76804	Human PRO polynuc
17	2265	83.7	2764	25	ABX16644	Human cDNA encodin
18	2220.5	82.1	1917	21	AAA37848	Human obesity prot
19	2220.5	82.1	3099	20	AAV99912	Human staloathesin
20	2220.5	82.1	3099	20	AAV99912	Human staloathesin
21	2197.5	81.2	2295	21	AAA80610	Human CD33-like se
22	2142.5	79.2	2954	24	ABK43361	DNA encoding stail
23	2142.5	79.2	2954	24	ABK43361	DNA encoding stail
24	1929.5	71.3	2823	24	ABK43362	DNA encoding stail
25	1929.5	71.3	2823	24	ABK43362	DNA encoding stail
26	1728	62.9	1824	24	ABK43363	Siglec-BMS-13a-hig
27	1680.5	62.1	2154	24	ABO72566	DNA encoding stail
28	1633.5	56.7	1029	23	AA580254	Human MDR1 encodin
29	1517.5	55.9	2061	24	ABO86144	DNA encoding novel
30	1507.5	55.7	2058	25	ABO53168	Novel human gene.
31	1454.5	53.8	2052	24	ABK43375	Human Siglec-12 DN
32	1443	53.3	2004	24	ABO86145	Siglec-BMS-13a-hig
33	1396.5	51.6	1344	21	AAA80619	Novel human gene.
34	1336	49.4	1974	23	AA580252	Human secreted pro
35	1329	49.1	1859	23	AA584407	DNA encoding novel
36	1270.5	47.0	1578	23	AA580253	DNA encoding novel
37	947	35.0	1592	24	AA38935	Siglec-L coding c
38	924	34.1	1473	24	ABA90353	Human polynucleoti
39	916	33.9	1736	24	AAO37892	Siglec-like gene (
40	916	33.9	1860	24	ABA90352	Human polynucleoti
41	909	33.6	2197	22	AAO08641	Human kinase (PKIN
42	909	33.6	2139	22	AAE76851	Human secreted pro
43	900	33.3	1554	24	ABK43364	DNA encoding stail
44	888	32.8	1597	20	AAK17773	SAF-2 polypeptide
45	888	32.8	2900	20	AAK17772	SAF-2 polypeptide

ALIGNMENTS

RESULT 1
ID AAA37847 standard; DNA: 1536 BP.
AC AAA37847;
XX
XX 12-FEB-2001 (first entry)
DE Human obesity protein binding protein-2 homologue coding sequence #1.
XX
XX Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
KM obesity-related disorder; therapy; ds.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 1..1536
FT CDS

with off.iation

FT /tag= a
FT /product= hOB-BP2h
XX WO200059942-A2.
XX 12-OCT-2000.
XX 22-MAR-2000; 2000WO-US06682.
XX 02-APR-1999; 99US-0127667.
XX (ELIL) LILLY & CO ELI.
XX Su EW, Wei J;
XX WPI: 2000-664992/64.
XX P-PsDB: AAY97542.
XX
XX New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders
XX
XX Claim 3; Page 85; 92pp; English.

CC This sequence encodes a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for the recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides.

SO Sequence 1536 BP; 354 A; 487 C; 401 G; 294 T; 0 other;

Alignment Scores:
Pred. No.: 2,47e-185 Length: 1536
Score: 2706.00 Matches: 512
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-937-636-3 (1-512) x AAA37847 (1-1536)

QY 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20
DB 1 ATGCTACTGCACGCTGCTCTCTCGTGGTGGGCGGTCCAGGCAATGAGTGGAGA 60
QY 21 PheTrpIleArgValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro 40
DB 61 TTCTGAGATACGACGACAGAGTCAAGTGTGTCGGGAGGCGCTGTGCATCTCTGCGCC 120
QY 41 CysSerPheSerTrpProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60
DB 121 TGTCTTTCTCTACCCCGACAGACTGACAGAGGTATACCCAGCTTAATGCTACTGG 180
QY 61 PheIysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
DB 181 TTCAAAGCAGTACGACGACACCAACAGGCTGCTCTGGCCACAAACACACAGAGTGA 240
QY 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
DB 241 GAGGTGGAATGAGACCCGGGGCGGATTCACAGCTCACTGGGATCCCGCAAGGGGAGAC 300
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
DB 301 TGTCTCTGTGATCAGACGCGCAGATGCAAGATGAGTCAAGTACTTCTTTCGGGTG 360

QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPheLeuLysValThr 140
DB 361 GAGAGAGGAAGCTATGTGAGATTAATTTATGAAAGATGGTCTTTCTTAAGATACAA 420
QY 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160
DB 421 GCCCTGACTCAGAAAGCTGATGTCTACATCCCGAGAGACCCGGAGCCGGGGAGCGGTG 480
QY 161 ThrValIleCysValPheAsnTrpAlaPheGluGlyCysProProPheSerPheSerTrp 180
DB 481 ACGGTCACTGTGTGTTAACTGGGCTTTGAGGAAATGTCCACCCCTTCTTCTCTGG 540
QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
DB 541 ACGGGGGCTGCCCTCTCTCCCAAGAGAACCAACCAACAGCTTCCACTTCTCAGTCTC 600
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
DB 601 AGCTTACAGCCCAAGACCCAGAGACAGACAGACAGACCTCACTGATGTGACTTCTCC 660
QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
DB 661 AGAAAGGTGTGACCGCACAGAGAGACCGTCCGACTCCGTGTGGCTTATGCCCCAGAGAC 720
QY 241 LeuValIleSerIleSerArgAspAsnThrProAspProProGluAsnLeuArgValMet 260
DB 721 CTGTGTATACATTTTACGTGTGACACACACGCCAGATCTTCCAGAAACCTGAGAGTATG 780
QY 261 ValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuProVal 280
DB 781 GTTCCCAAGCAAGACAGACAGTCTCGAAACCTTGGAAAGGACAGTCTTCCACAGTA 840
QY 281 LeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArgLeu 300
DB 841 CTGAGAGCCCAAGACCTGT 900
QY 301 SerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyValLeu 320
DB 901 AGCTGAGACCCAGAGGGGACAGGTGTGTGAGCCCTCCAGCCCTCAGACCCCGGGTCTGT 960
QY 321 GluLeuProArgValAlaGlnValGlnHisGlnGlyLuePhePheCysHisAlaArgHisPro 340
DB 961 GAGTGTGCTGTGGTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1020
QY 341 LeuGlySerGlnHisValSerLeuSerLeuSerValHisTyrLysGlyLeuIleSer 360
DB 1021 CTGGGCTCCAGACAGCTCTCTCTCAGCCCTCGCTGACCATTAAGAAAGGAGCATCTCA 1080
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DB 1201 CCCAGGTTCTCCGGCAGACAGACAGATCTGTGATTAACATCAATGATGTGCCAGCGTGGC 1260
QY 421 ProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440
DB 1261 CCCCTGGTGTGAAGCGGAATCAAAAGCCACCAACCACTCTGGACCCCTTCTTCCA 1320
QY 441 ProGlyAlaProSerProGluSerLysAsnGlnLysGlnTyrGlnLeuProSer 460
DB 1321 CCAAGTGTCTCTCTCCCAAGATCAAAAGAGAACCAAGAAAGAGTATCACTTCCAGT 1380
QY 461 PheProGluProLysSerSerThrGlnAlaProGluSerGlnGluGluLeu 480
DB 1381 TTCCAGAAACCAATATCATCATCAAGCCCAAGATCCAGAGAGGCAAGAGAGAGTCTC 1440
QY 481 HisTyrAlaThrLeuAsnPheProGlyValArgProArgProGluAlaArgMetProLys 500


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Db      1078 TACACCTGCGAGGCGAGACAGGCTTGCTCCAGCAGCGAGCCCTGGACCTCTCTGTG 1137
QY      253 -----ProProGluAsnLeuAlaArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
Db      1138 CAGTATCTCTCCAGAAACCTGAGAGTGTGTTCCCAAGCAAAACAGACAGTCTCTGGAA 1197
QY      271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyInsSerLeuCyLeuValCys 290
Db      1198 AACCTGGAGACGGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTTGCTGCTGTGT 1257
QY      291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
Db      1258 GTCAACACAGACAGCCCGCCAGCAGCTGAGTGGACCCAGAGGGGAGAGTCTGTAGC 1317
QY      311 ProSerGlnProSerAspProGlyValLeuGluLeuProAlaArgValGlnValGluSer 330
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QY      351 SerValHisTyr----- 354
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QY      354 ----- 354
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QY      354 ----- 354
Db      1558 GAGTGTGTGAGGGGAGACAGACAGCCAGACTCTTTCGAGGTACACCCCGAGCTCAGCCGG 1617
QY      354 ----- 354
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QY      355 -----Lys 355
Db      1678 TGTGAGGCTGGAACGTCCATGGGGCCCGAGAGTGCATCCCTGCAGCTCCCGAATTAAG 1737
QY      356 LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla 375
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QY      376 LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGln 395
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QY      396 ThrGluThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal 415
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QY      416 ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro 435
Db      1918 GTCCCGAGCGGCTGGCCCTGCTGCTCAGAAACGGGATCAGAAACCCACCAACAGAGTCT 1977
QY      436 ArgThrProLeuProProGlyAlaProSerProGlnSerLysLysAsnGlnLysGln 455
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QY      456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu 475
Db      2038 TATCAGTGGCCAGTTCCAGAAACCAATCATTCACCTAAGCCCGAGATCCAGGAG 2097
QY      476 SerGlnGluGlnLeuHisTyrAlaThrLeuAsnPheProGlyAlaArgProArgProGlu 495
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QY      496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512

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Db      2158 GCCCGATGCCAGAGCGACCCAGCGGATTTATGCAAGTCAAGTCCAA 2208
RESULT 3
ABK43373
ID      ABK43373 standard; cDNA: 3024 BP.
XX
AC      ABK43373;
XX
DT      05-JUN-2002 (first entry)
XX
DE      DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2.
XX
KW      Human; sialic acid-binding Ig-related lectin; SigLEC; asthma;
KW      immune system disease; leukaemia; allergy; inflammatory disease;
KW      tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KW      psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200208257-A2.
XX
PD      31-JAN-2002.
PF      20-JUL-2001; 2001WO-US23082.
PR      21-JUL-2000; 2000US-220139P.
PX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      Longphre M, Chang H, Whitney G;
XX      WPI: 2002-241565/29.
XX      P-PsDB: AA087087.
XX
PT      Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
PT      molecules useful for treating immune system diseases such as asthma,
PT      leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
PT
XX
PS      Example 11; Figure 6; 20pp; English.
XX
XX      The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
XX      related lectin) protein (I). Pharmaceutical compositions comprising (I)
XX      are useful for treating immune system diseases such as asthma, leukaemia
XX      or other allergic or inflammatory diseases. Extracellular domains of (I)
XX      represent potential markers for screening, diagnosis, prognosis,
XX      follow-up assays, and imaging methods. (I) is useful as a target for
XX      drugs which inhibit inflammation, tissue damage and remodeling in
XX      asthma, and inflammatory diseases such as allergic rhinitis,
XX      osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
XX      conjunctivitis, etc. (I) is also useful for monitoring the course of
XX      disease or disorders, and for identifying agents that bind with and/or
XX      modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
XX      molecules (II) encoding (I) are useful in diagnosis and/or prognosis
XX      methods, and to detect the presence and/or amount of SIGLEC-BMS
XX      nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
XX      (II) are useful as nucleic acid probes are useful for screening genomic
XX      library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
XX      number is determined for detecting diseases or disorders associated with
XX      SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
XX      used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
XX      and in diagnostic imaging technology. ABK43360-ABK43411 represent
XX      human SIGLEC coding sequences and PCR primers of the invention.
XX
SQ      Sequence 3024 BP; 699 A; 933 C; 790 G; 602 T; 0 other;

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Alignment Scores:

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Pred. No.: 5,94e-176
Score: 2580.50
Percent Similarity: 73.31%
Best Local Similarity: 73.17%
Query Match: 95.36%
Length: 3024
Matches: 510
Conservative: 1
Mismatches: 1
Indels: 185

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DB:		24	Gaps:	2
US-09-937-G36-3 (1-512) x ABR43373 (1-3024)				
OY	1	MethLeuLeuProLeuLeuLeuSerSerLeuLeuLysGlySerGlnAlaMetAsnGlyArg	20	
Dd	129	ATGCTACTGCACAGCGTGTCTCCCTCCTGGCGGGGTCCCAAGGCTATGGATGGGA	188	
OY	21	PheTrpIleArgValGInGlySerValMetValProGluGlyLeuCysIleSerValPro	40	
Dd	189	TTCCTGGATTACGAGTGACAGACTAGTATGGTGGCGAAGGCCCTGTGCTATCTGTGCC	248	
OY	41	CysSerPheSerTyProArgGlnAspTrpThrGlySerThrProAlaTyrgLYTYrTrp	60	
Dd	249	TGCTCTTTCTTCCTACCCTCCGACAAGACTGACAGAGGCTTACCCTCAGCTTATGGCTACTGG	308	
OY	61	PheValAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	80	
Dd	309	TTCAAACAGAGACTGAGACAAACCAAGGCTGCTCTGTGGCCACAACACACAGAATCGA	368	
OY	81	GluValGlnMetSerTrpArgGLyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	100	
Dd	369	GAGGTGGAAATGACACACCCGGGGCGGATTCACAGTCACTGGGGATCCCGCCAAAGGGGAAC	428	
OY	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGlySerGlnTyrrPhePheArgVal	120	
Dd	429	TGCTCCCTTGGTGATCAGAGACGGCCAGATGAGATGAGTACAGTACTTCTTCGGGTG	488	
OY	121	GluArgGlySerTyrrValArgTyrrAsnPhenMetAsnAspGlyPhePheLeuLysValThr	140	
Dd	489	GAGAGAGGAAGCTATGTGACATATAATTAATTCATGCAACGATGGGTTCTTCCTAAAAGTAA	548	
OY	141	AlaLeuThrGlnLysProAspValTyrrIleProGluThrLeuGluProGlyGlnProVal	160	
Dd	549	GCCCTGACTCAAGAAAGCTGATGTACTATCCCAGAGACCTTGAGAACCCGGGACAGCGGTG	608	
OY	161	ThrValIleCysValPheAsnTrpAlaPheGluLucysProProPheSerPheSerTrp	180	
Dd	609	ACGCTCATCTGTGTGTTAACTGGGCGCTTGAGAAATGTCACACCCCTCTTCTTCCTCGG	668	
OY	181	ThrcLYlAlaIleLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	200	
Dd	669	ACGGGGGCTGCCCTCTCTCCCAAGGAACCAACCAAGACCTCCACATTCACGTGCTC	728	
OY	201	SerPheThrProArgProGlnAspHisAspPheAsnLeuThrCysHisValAspPheSer	220	
Dd	729	AGCTTCACGCCACCAACCCACGACCAACACCGACCTCACCTCGCATGTGACTTCTCC	788	
OY	221	ArgLYslLyValSerAlaGlnArgThrValArgLeuArgValAlaTyrrAlaProArgAsp	240	
Dd	789	AGAAAGGGTGTGACGCGACAGAGAGACCGTCCGATCCGTGTGGGCTATGGCCCCAGAGAC	848	
OY	241	LeuValIleSerIleSerArgAspAsnThrProAsp-----	252	
Dd	849	CTTGTTATACACTTTCACGTGACACACGCGCACCCCTTGAGCCCCAGGGAAT	908	
OY	252	-----	252	
Dd	909	GTCCCATACCTGGGAAGCCCAAAAAGGCAAGTTCTCGGGGCTCTGTGCTGACAGC	968	
OY	252	-----	252	
Dd	969	CAGCCCTCGCACACTGAGCTGGGTCTCGAGAAACAGATCGTCTCTGTCCTCATCC	1028	
OY	252	-----	252	
Dd	1029	TGGGGCCCTTAGACCCCTGGGGCTGAGACTGCCCGGGGTGAAGGCTGGGATTCAGGGCC	1088	
OY	252	-----	252	
Dd	1089	TACACCTGCGCAGGGGAGACAGAGCTTGGGTCTCCAGCAGCGACGCCCTGTCTGTG	1148	
OY	253	-----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	270	

Db	1149	CAGTATCTCCAGAGAACCTGAGAGTATGATTGTTCCCAACCAAAACAGACAGCTCTGAA	1208
QY	271	AsnLeuLysAsnGlyThrSerLeuProValLeuGluGlyInsLeuCysLeuValCys	290
Db	1209	AACCTTGGAAGGACAGCTCTCTCCAGTACTGGAGGGCCAAAGCTGTGCTGGTCTGT	1268
QY	291	ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	310
Db	1269	GTCACACACAGACACCCCCCAGCCAGGCTAGCTGAGACCCAGAGGGGACAGGTTCTAGC	1328
QY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu	330
Db	1329	CCCTCCAGCCCTCAGACCCCGGGGGTCTGGAGCTGCTGGGTTCAAGTGGACACAGAA	1388
QY	331	GlyLeuIleuThrCysHisHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1389	GGAGAAGTTCAACCTTCACAGCTCGGACCCACTGGGGCTCCAGACAGCTCTCTCAGCTC	1448
QY	351	SerValHisIleIle	354
Db	1449	TCCGTGCATCTACTCCCGGAAGCTCTGGGCCCTCTGCTCTCTGGAGAGCTGAGAGGCTG	1508
QY	354	-----	354
Db	1509	CATGCGAGCTGCTCTCCACAGGCCAGCCGCCCTCTCTGCGCTGTGGCTTGGGGAG	1568
QY	354	-----	354
Db	1569	GAGCTGCTGAGGGGGAACAGCAGCCAGGACTCTTCGAGGTACACCCCAAGCTACGCCGG	1628
QY	354	-----	354
Db	1629	CCCTGGGCCAACAGCTCCCTCTAGCTCTCATGGAGGCTCAGCTCCGGCTCAGGCTCCGC	1688
QY	355	-----Lys	355
Db	1689	TGTGAGGCGTGGAAAGCTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG	1748
QY	356	LysGlyLeuLeuIleSerThrAlaPheSerAsnGlyValaPheLeuGlyIleGlyIleThrAla	375
Db	1749	AAGGAGCTCATCTCAACGGCATTTCTCCACCGACGAGCTTCTGGGAAATCGGATCAGCGCT	1808
QY	376	LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGln	395
Db	1809	CTTCTTTTCCCTCTGCTGCGCCCTGATCATCTGAAGATTCTACCGAAGAGAGGACTCAG	1868
QY	396	ThrGluThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal	415
Db	1869	ACAGAAACCCCGAGGCGCAGGTTCTCCCGGACAGCAGATCTCGATTACATCAATGTG	1928
QY	416	ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro	435
Db	1929	GTCGCCAGCGGTGGCCCCCTGGCTCAAAAGGGATAGAAAGCCACACCAAAAGTCTT	1988
QY	436	ArgThrProLeuProProGlyAlaProSerProLeuSerLysAsnGlnLysGln	455
Db	1989	CGAGACCCCTTCCACACGAGTGTCTCCCTCCCAATACTMAAGAAACACGAAAAACAG	2048
QY	456	TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu	475
Db	2049	TATCAGTTGGCCCACTTTCACGAAACCAAAATCATCACTCAACGCCCAAGATCCACAGAG	2108
QY	476	SerGlnGluGluSerHisIleIleThrLeuAsnPheProGlyValaArgProArgProGlu	495
Db	2109	AGCCAAAGAGGAGCTCCATTATGCCAGCTCAACTTCCAGGCGTCAGACCCAGGCTGAG	2168
QY	496	AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	512
Db	2169	GCCCGGATGCCCAAGGCGACCCAGCGGATTATGCAGAAAGTCAAGTTCAA	2219

RESULT 4
ABK43360

Db 1035 AACCTGGGAGGACGCTCTCTCCAGTACTGGAGGCCAAAGCCTGTGCTGTCTGT 1094
QY 291 VAlThrHIsSerSerProProAlaArGLeuSerTTPThGlaArgGlyGlnValLeuSer 310
Db 1095 GTTACACACACAGACGCCCCCACCAGGCTGAGCTGGACCCAGAGGGAGAGGTTCTGACC 1154
QY 311 ProSerGlnProSerAspProGluValLeuGlnLeuProArgValGlnValGlnGln 330
Db 1155 CCTCCAGCCTTCAGAGACCCGGGGTCTGGAGTCCCTCGGGTTCAATGGAGCGCAGA 1214
QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
Db 1215 GGAGAGTTCACCTGGCACCGCTGGCACCCACTGGGGTCTCCACACGCTCTCTCTCAAGCCTC 1274
QY 351 SerValHisTyrLysLysGlyLeuLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
Db 1275 TCCGTCGACTATAGAGAGGACTCATCTTAAGGCACTTCTCCAGCGAGCGTTCTGGGA 1334
QY 371 ILeGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390
Db 1335 ATCGGCATCAGCGCTCTTCTTTCTCTGCTGCTGGCCCTGATCATGTAAGATTCTACCG 1394
QY 391 LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu 410
Db 1395 AAGAACGGACTCAGACAGAAACCCCGAGGCCAGAGTTCTCCCGGACAGCAGATCTTG 1454
QY 411 AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
Db 1455 GATTACATCATGTGTTCCCGACGGCTGGCCCCCTGGCTCAGAGCGGATCAGAGGCC 1514
QY 431 ThrProAsnSerProArgThrProLeuProProGluAlaProSerProGluSerLysLys 450
Db 1515 ACACCAACAGTCTCTGGACCCCTCTCCACAGGAGTCTCCCTCCACAAATCAAGAAG 1574
QY 451 AsnGlnLysLysGlnThrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
Db 1575 AACCGAATAAACAGATCATGTTGCCATTGCCAGAACCCAAATCATCCACTCAAGCC 1634
QY 471 ProGluSerGlnGluSerGlnGluLeuHisTyrAlaThrLeuAsnPheProGluVal 490
Db 1635 CCAGAAATCCAGAGAGCCAAAGAGAGCTCCATTATGCCAGCTCACTTCCAGGCGTTC 1694
QY 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
Db 1695 AAGACCCAGGCTGAGAGCCCGGATGCCAAAGGCGACCCAGCGGATATCAGAGAATCAG 1754
QY 511 PheGln 512
Db 1755 TTCCAA 1760

RESULT 5
AAZ34109
ID AAZ34109 standard; cDNA: 2764 BP.
XX AAZ34109;
AC
XX
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO940 nucleotide sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
XX
XX WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
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PR 12-MAR-1998; 98US-0077791.
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PR 17-MAR-1998; 98US-0040220.
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PR 01-APR-1998; 98US-0080327.
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PR 21-APR-1998; 98US-0082700.
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PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
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PR 05-MAY-1998; 98US-0084366.
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PR 07-MAY-1998; 98US-0084600.
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PR 13-MAY-1998; 98US-0085323.
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PR 13-MAY-1998; 98US-0085339.
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PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086352.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087206.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DX WPI; 1999-551358/46.
DR P-PSDB; AAY41724.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX Claim 2; Fig 92; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23891 to
CC AA23438, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,54e-153 Length: 2764
Score: 2265.00 Matches: 450
Percent Similarity: 74.92% Conservative: 1
Best Local Similarity: 74.75% Mismatches: 3
Query Match: 83.70% Indels: 148
DB: 20 Gaps: 2
US-09-937-636-3 (1-512) x AA234109 (1-2764)
QY 1 MetLeuLeuProLeuLeuLeuSerLeuLeuGlySerGlnAlaMetAspGlyArg 20
DB 46 ATGCTACTGCGACCTGCTGCTCTCTGCTGCGGCGGCTCCAGGCTATGAGTGGAGA 105
QY 21 PheTrpIleArgValGlnGlnuserValMetValProGlnGlyLeuCysIleSerValPro 40
DB 106 TTTCGATACGAGTGCAGGAGTGCATGATGTCGCGAGGCGCTGTCATCTCTGTCGCC 165
QY 41 CysSerPheSerTrpProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60
DB 166 TGCTCTTCTCTCTACCCCGACAAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 225
QY 61 PheIleAlaValThrGlnTrpThrThrGlyAlaProValAlaThrAsnHisGlnSerArg 80
DB 226 TTCAAAACAGTGAAGTGAACAACCAAGGCTCTCTGCGCACAAACACAGAGTGA 285
QY 81 GluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaTyrGlyAsn 100
DB 286 GAGGTGAATGAGCACACCGGGGCGCATTCAGCTCACTGGGAGTCCCGCAAGGGAGAC 345
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120

DB 346 TGCTCTGTCGATCAGAGAGACCGCAGATGAGAGTACAGTACTCTTCGGGGTG 405
QY 121 GluArgGlySerTrpValArgTyrAsnPheIleAsnAspGlyPhePheLeuValThr 140
DB 406 GAGAGAGAAAGCTATGTGATCATTAATTTCAATGAAACGATGGGTTCTTTAAAGTAAACA 465
QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
DB 465 ----- 465
QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGluCysProProPheSerPheSerTrp 180
DB 465 ----- 465
QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
DB 466 -----GTCCTC 471
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
DB 472 AGCTTCAGCGCCACACCCCGAGACACACACGACGACCTCACTGCTGAGACTTCTCC 531
QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
DB 532 AGAAGGGTGTGACCGACAGAGACCGCTCCGACTCCGTCGTGGCCCTATGCCCCAGAGAC 591
QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
DB 592 CTGTGTATACGATTTTACGTGACGACACACGACGCCACCTCGACGCCACCGAGGAAT 651
QY 252 ----- 252
DB 652 GTCCCATACCTCGAAGGCCCAAAAGGCCAGTTCCTGGGGCTCTCTGTGCTGACAGC 711
QY 252 ----- 252
DB 712 CAGCCCCGTGCACACTGAGCTGGTCTCGACAGAACAGAGTCTCTCTGTCCTCCATGCC 771
QY 252 ----- 252
DB 772 TGGGGCCCTAGACCCCTGGGGCTGAGACTGCCGGGGTGAAGCTGGGGATTCAAGGCCC 831
QY 252 ----- 252
DB 832 TACACCTGCGGAGCGAAGACAGCTTGCTGCCAGCAGCGACCTGACCTCTCTGTG 891
QY 253 -----ProProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
DB 892 CAGTATCTCCAGAGAACCTGAGAGTGTGTTCCCAAGCAACAGAGACAGTCTCGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuValCys 290
DB 952 AACCTTGGGAACGCGACGCTCTCTCCAGTACTGAGGAGCCCAAGACCTGTGCTGTGT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
DB 1012 GTCACACACAGACACCCCGCAGCGCTGAGTGGAGCCAGAGAGGAGACAGTCTCTGAGC 1071
QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnHisGln 330
DB 1072 CCCCTCCAGGCCCTCAGACCCCGGGGCTCTGAGCTGCTCGGGTTCAAGTGGACAGAA 1131
QY 331 GlyIlePheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
DB 1132 GGAGAGTTTCACTTCCACCGCTCGGACCCACTGGGCTTCCACGACGCTCTCTCAGGCTC 1191
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DB 1192 TCGGTGACATATAAGAGGAGCATCATCTCAAGGCAATTTCCAAAGGAGGATTTCTGGA 1251
QY 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390


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QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
Db 466 -----GTCGTC 471
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
Db 472 AGCTTCACGCCACAGCCAGGAGCCACACACCGACCTCAGCTGATGAGCTTCGCC 531
QY 221 ArgGlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaIleValAlaProArgAsp 240
Db 532 AGAAGGGGTGTGACGCGACAGAGGACGCTCGACTCGGTGGCTATGCCCCAGAGAC 591
QY 241 LeuValIleSerIleSerArgAspAsnThrProasp ----- 252
Db 592 CTTCGTATACAGATTTCACGTGACACACGCGACGCCCTGGAGCCCCAGCCAGGAAT 651
QY 252 ----- 252
Db 652 GTCCCATACCTGAGAGCCCAAAAGGCCAGTTCCTCGGCGCTCTGTGCTGACAGC 711
QY 252 ----- 252
Db 712 CAGCCCCCTGCCACACTGAGCTGGGCTCCGACAGACAGAGTCTCTCTGCTCCATCCC 771
QY 252 ----- 252
Db 772 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 831
QY 252 ----- 252
Db 832 TACACCTGCCAGGAGGAGAACAGGCTTGCTCCAGACGAGCGAGCCCTGACCTCTCTGTG 891
QY 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
Db 892 CAGTATCTCCAGAGAACTGAGAGTATGTTTCCCAAGCAAGACAGACAGTCTCGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyIleSerLeuValLeuValCys 290
Db 952 AACCTGGAGAGCGACGCTCTCCAGTACTGAGGAGCCAAAGCCTGCTGCTGTGTGT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerThrGlnArgGlyGlnValLeuSer 310
Db 1012 GTCCACACAGCAGCCCCCAGCCAGGCTGAGTGGACCCAGAGAGGAGACAGGTTCTAGC 1071
QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnGlu 330
Db 1072 CCTCCAGGCCCTCAGACCCCGGGGCTCTGAGCTGCTGGGTTCAAGTGGAGCAGAA 1131
QY 331 GlyIleuPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
Db 1132 GGAGAGTTCACGTGCGCAGCGCTCGCACCCACTGGGCTCCAGCAGCTCTCTCAGCCTC 1191
QY 351 SerValHisThrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
Db 1192 TCGGTGACTATAGAGGAGCATCTCAACGCGATCTCCACAGGAGGAGGTTCTGGGA 1251
QY 371 IleGlyIleThrAlaLeuPheLeuPheCysLeuAlaLeuIleIleMetLysIleLeuPro 390
Db 1252 ATGGGCAATCAGGCTCTTCTTTCCTTCTGCTGCTGCTGCTGATCATCAAGAGATTCTACCG 1311
QY 391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu 410
Db 1312 AAGAGACGAGCTCAGACAGAAACCCGAGGCCAGGTTCTCCGGCAGACAGATCTCTG 1371
QY 411 AspTyrIleAsnValProThrAlaGlyProLeuAlaGlnLysAspGlnGlnLysAla 430
Db 1372 GATTACATCAATGAGGCTCCGAGCGCTGGCCCTGCTCAGAGCGGAATCAGAAAGGCC 1431
QY 431 ThrProAsnSerProArgThrProLeuProGlyValAlaProSerProGlnSerLysLys 450
Db 1432 ACACCAAAACAGTCTCTGAGACCCCTCTCCACAGGCTCTCTCTCCAGATCAAGAGAG 1491
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QY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGlnProLysSerSerThrGlnAla 470
Db 1492 AACCAAGAAAAGCATATCATGTTGCCAGATTCACAGACCCAAATCATCATCAAGGCC 1551
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Db 1552 CCAGAAATCCCGAGGAGACCAAGAGAGAGCTCATATATGCGCACTTCCAGGGGCTC 1611
QY 491 ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
Db 1612 AGACCCAGGCTCGAGGCCGGATGCCCAAGGGCACCCAGGGGAGTATGACAGATCAAG 1671
QY 511 PheGln 512
Db 1672 TTCCAA 1677
RESULT 7
AAS45983
ID AAS45983 standard; cDNA; 2764 BP.
AC AAS45983;
XX 18-DEC-2001 (first entry)
DE 18-DEC-2001 (first entry)
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN NC020168848-A2.
XX
PD 20-SEP-2001.
XX
PE 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
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QY 252 ----- 252
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Db 892 CAGATCTCTCCAGAACTGAGAGTGATGTTCCCAAGCAAAACAGACAGTCTCGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuGlyValCys 290
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QY 291 ValThrHisSerSerProProAlaArgLeuSerThrThrGlnArgGlyGlnValLeuSer 310
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QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
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DT 19-MAY-2003 (first entry)
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KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cytosolic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.
XX
OS Homo sapiens.
XX
PN US2003036156-A1.
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
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Best Local Similarity: 74.75% Mismatches: 3
Query Match: 83.70% Indels: 148
DB: 25 Gaps: 2

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DB 46 ATGCTACTGCGACATGCTGCTGCTCCCTGCGCGGATCCACAGGCTATGATGGAGA 105
QY 21 PheTrpIleArGValGInGInSerValMetValProGluGlyLeuCySIIleSerValPro 40

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Db      106 TTCTGATACGATGTCAGAGTCAGTATGATGTCGCGAGGCGCTGTGCATCTGTGCCC 165
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Qy      121 GluArgGlySerTyrValArgTyrAsnPhMetAsnAspGlyPhePheLysValThr 140
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Db      465 ----- 465
Qy      161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp 180
Db      465 ----- 465
Qy      181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
Db      466 -----GTGCTC 471
Qy      201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
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Qy      221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
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RESULT 10
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20-MAY-2003 (first entry)
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Human; secreted protein; transmembrane protein; cytosolic;
KW gene Therapy; TNF-Agonist-Alpha; Chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW gene; ss.
OS Homo sapiens.
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PR 08-APR-1998: 98US-081049P.
PR 08-APR-1998: 98US-081070P.
PR 09-APR-1998: 98US-081195P.
PR 15-APR-1998: 98US-081838P.
PR 21-APR-1998: 98US-082569P.
PR 22-APR-1998: 98US-082704P.
PR 22-APR-1998: 98US-082797P.
PR 28-APR-1998: 98US-083322P.
PR 29-APR-1998: 98US-083495P.

PR 29-APR-1998: 98US-083496P.
PR 29-APR-1998: 98US-083499P.
PR 29-APR-1998: 98US-083559P.
PR 05-MAY-1998: 98US-084356P.
PR 06-MAY-1998: 98US-084414P.
PR 07-MAY-1998: 98US-084639P.
PR 07-MAY-1998: 98US-084640P.
PR 07-MAY-1998: 98US-084643P.
PR 15-MAY-1998: 98US-085579P.
PR 15-MAY-1998: 98US-085580P.
PR 15-MAY-1998: 98US-085582P.
PR 15-MAY-1998: 98US-085700P.
PR 18-MAY-1998: 98US-086023P.
PR 22-MAY-1998: 98US-086392P.
PR 22-MAY-1998: 98US-086486P.
PR 28-MAY-1998: 98US-087098P.
PR 28-MAY-1998: 98US-087208P.
PR 02-JUN-1998: 98US-087609P.
PR 02-JUN-1998: 98US-087759P.
PR 03-JUN-1998: 98US-087827P.
PR 04-JUN-1998: 98US-088025P.
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PR 04-JUN-1998: 98US-088033P.
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PR 05-JUN-1998: 98US-088167P.
PR 05-JUN-1998: 98US-088202P.
PR 05-JUN-1998: 98US-088212P.
PR 05-JUN-1998: 98US-088217P.
PR 09-JUN-1998: 98US-088655P.
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PR 10-JUN-1998: 98US-088811P.
PR 10-JUN-1998: 98US-088824P.
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PR 11-JUN-1998: 98US-088861P.
PR 11-JUN-1998: 98US-088863P.
PR 11-JUN-1998: 98US-088876P.
PR 12-JUN-1998: 98US-089050P.
PR 12-JUN-1998: 98US-089105P.
PR 16-JUN-1998: 98US-089512P.
PR 16-JUN-1998: 98US-089514P.
PR 17-JUN-1998: 98US-089538P.
PR 17-JUN-1998: 98US-089598P.
PR 17-JUN-1998: 98US-089653P.
PR 18-JUN-1998: 98US-089908P.
PR 19-JUN-1998: 98US-089952P.
PR 22-JUN-1998: 98US-090246P.
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PR 24-JUN-1998: 98US-090429P.
PR 24-JUN-1998: 98US-090435P.
PR 24-JUN-1998: 98US-090444P.
PR 24-JUN-1998: 98US-090461P.
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PR 25-JUN-1998: 98US-090676P.
PR 25-JUN-1998: 98US-090688P.
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PR 25-JUN-1998: 98US-090690P.
PR 25-JUN-1998: 98US-090694P.
PR 25-JUN-1998: 98US-090695P.
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PR 26-JUN-1998: 98US-090862P.
PR 26-JUN-1998: 98US-090863P.
PR 26-JUN-1998: 98US-091010P.
PR 01-JUL-1998: 98US-091359P.
PR 01-JUL-1998: 98US-091544P.
PR 02-JUL-1998: 98US-091478P.
PR 02-JUL-1998: 98US-091486P.
PR 02-JUL-1998: 98US-091626P.

QY 451 AsnGlnLysLysGlnIrrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
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Db 1492 AACCCAGAAAAAGCATGATGTTGCCAGATTGCCAGAACCCAAATCATCTCAACGCC 1551
QY 471 ProGluSerGlnIrrGlnLeuHisTyrAlaThrLeuSerPheProGlyVal 490
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Db 1552 CCAGAAATCCAGAGAGCCAAAGAGAGCTTCATTATGCCACGCTCAACTTCCAGAGCGCTC 1611
QY 491 ArgProArgProGluAlaArgMetProLysGlnIrrGlnAlaSprYrAlaGluValLys 510
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Db 1612 AGACCCAGGCGCTGAGGCGGATGCCCCAAGGCAAGCCAGGCGGATTTATGCAAGATCAAG 1671
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Db 1672 TTCCA 1677
RESULT 11
ACA05758
ID ACA05758 standard; cDNA; 2764 BP.
XX
AC ACA05758;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #59.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX
OS Homo sapiens.
XX
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-0194423.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.

PR 29-AUG-2001; 2001WO-US27099.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 03-MAR-1999; 99US-0254311.
PR 14-MAY-1999; 99US-0311832.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 18-OCT-1999; 99US-0403297.
PR 12-NOV-1999; 99US-0423844.
PR 22-AUG-2000; 2000US-0644848.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 08-NOV-2000; 2000US-0709238.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 05-JUN-2001; 2001US-0874503.
PR 18-JUL-2001; 2001US-0908827.
PR 30-JUL-2001; 2001US-0918585.
PR 06-AUG-2001; 2001US-0929404.
PR 13-AUG-2001; 2001US-0929404.
PR 16-AUG-2001; 2001US-0931836.
PR 28-AUG-2001; 2001US-0941992.
PR 04-SEP-2001; 2001US-0946374.
PR 15-JAN-2002; 2002US-0052586.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
PI
XX
DR WPI: 2003-332039/31.
DR P-PSDB; AB067464.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acids,
PT useful in gene therapy. In chromosome and gene mapping, as chromosome
PT markers, in tissue typing, and in chromosome identification
XX
XX
PS Claim 2; Fig 117; 706pp: English.

XX
XX The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention.
XX

SQ Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other;

Alignment Scores:

Pred. No.: 2.54e-153 Length: 2764
Score: 2265.00 Matches: 450
Percent Similarity: 74.92% Conservative: 1

KW cardiant: gene; ss.
 XX Homo sapiens.
 OS
 XX US2002169284-A1.
 PN
 XX
 PD 14-NOV-2002.
 PF 16-OCT-2001; 2001US-0978697.
 XX
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 PR 07-OCT-1998; 98WO-US21141.
 PR 20-NOV-1998; 98WO-US24855.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12552.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 22-MAR-2001; 2001WO-US09552.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 17-OCT-1997; 97US-062250P.
 PR 03-NOV-1997; 97US-064249P.
 PR 13-NOV-1997; 97US-065311P.
 PR 21-NOV-1997; 97US-066364P.
 PR 10-MAR-1998; 98US-077450P.
 PR 11-MAR-1998; 98US-077633P.
 PR 11-MAR-1998; 98US-077641P.
 PR 11-MAR-1998; 98US-077649P.
 PR 12-MAR-1998; 98US-077791P.
 PR 13-MAR-1998; 98US-078004P.
 PR 20-MAR-1998; 98US-078886P.
 PR 20-MAR-1998; 98US-078910P.
 PR 20-MAR-1998; 98US-078936P.
 PR 20-MAR-1998; 98US-078939P.
 PR 25-MAR-1998; 98US-079294P.
 PR 25-MAR-1998; 98US-079656P.
 PR 27-MAR-1998; 98US-079663P.
 PR 27-MAR-1998; 98US-079664P.
 PR 27-MAR-1998; 98US-079689P.
 PR 27-MAR-1998; 98US-079728P.
 PR 30-MAR-1998; 98US-079786P.
 PR 30-MAR-1998; 98US-079920P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-0040220.

PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.
 PR 10-MAR-1999; 99US-0265686.
 PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380142.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvarioff E, Fong S, Gao W, Gerber H, Gertlisen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavani IJ, Kao SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tunnas D, Williams PM, Wood WI;
 DR WPI; 2003-288163/28.
 DR P-PSDB; AB061110.
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies
 XX
 PS Claim 2; Fig 92; 459pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC The present sequence encodes a human PRO polypeptide of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdIdentify.html.
 XX
 SQ Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.54e-153 Length: 2764
 Score: 2265.00 Matches: 450
 Percent Similarity: 74.928 Conservative: 1
 Best Local Similarity: 74.758 Mismatches: 3
 Query Match: 83.708 Indels: 148

[illegible]

Db	892	CAGTATCCCTCCAGAAACCTGAGTAGTGGTTTCCCAAGCAAAACGACAGTCCCTGGAA	951
QY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	290
Db	952	AACCTGGGGAAGCGACGCTCTCTCCAGTACTGAGAGGCGCAAGCGCTGTGCTGGTCTGT	1011
QY	291	ValThrHisSerSerProProAlaArgLeuSerThrPthrGlnArgGlyGlnValLeuSer	310
Db	1012	GTCACACACAGCAGCGCCCCCAGCCAGCGCTGAGCTGAGCCAGAGGGGACAGATTCTGAGC	1071
QY	311	ProSerGlnProSerAspProGlyValLeuGluGluLeuProArgValGlnValGlnHisGlu	330
Db	1072	CCCTCCACGCGCTCAGACCGCCCGGGGCTCTGGAGCTGCGCTCGGGTTCAAGTGGACACGAA	1131
QY	331	GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1132	GGAGAGTTTCACCTGCCAGCGCTCGGACCCACCTGGGCTCCAGCAGCTCTCTCAGCGCTC	1191
QY	351	SerValHisThrLeuGlyGlyGlyLeuLeuSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
Db	1192	TCCGCGCACTATAGAAAGGAGCTACTTCTCAACGCGATTTCTCCAAAGCGCTTTCTGGGA	1251
QY	371	IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro	390
Db	1252	ATCGGCATCAGCGGCTCTCTTCTTCTCTGCTGCGCCGATCATCATCATGAAATTCCTGACG	1311
QY	391	LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu	410
Db	1312	AAGAAGCGGAGCTCAGACAGAAACCCCGAGGCGCCAGGTTCTCCGCGCAGCAGCATCTCG	1371
QY	411	AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla	430
Db	1372	GATTACATCAATGTGTGCTCCGACGGCTGCGCCCGCTGAGAAAGCGAATCAGAAAGCC	1431
QY	431	ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys	450
Db	1432	ACACCAACAGCTCCCTGGAGCCCTCTCTCACAGAGTGTCTCTCCCGAAGTTCAAAGAG	1491
QY	451	AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla	470
Db	1492	AACGAGAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTCCATCCAGCC	1551
QY	471	ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal	490
Db	1552	CCAGATCTCCAGGAGAGGCAAGAGAGCTCCATTATGCCAGCTCAACTTCCAGGGCTC	1611
QY	491	ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys	510
Db	1612	AGACCCAGGCGCTGAGGCGCCGAGATGCCCAAGGCGACCCAGGCGGATTTATGCCAAGTCAAG	1671
QY	511	PheGln 512	
Db	1672	TTCCAA 1677	
RESULTE 13			
ID	ABX97802	standard; cDNA; 2764 BP.	
AC	ABX97802;		
XX	16-MAY-2003	(first entry)	
XX			
DE	Human PRO polynucleotide #59.		
XX			
XX	Human; PRO; gene; ss; cytosstatic; chromosome mapping; gene mapping;		
KW	protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;		
KW	chondrocyte differentiation; chondrocyte proliferation; tumour.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003032102-A1.		
XX			

PR	26-JUN-1998;	98US-090862P.
PR	26-JUN-1998;	98US-090863P.
PR	26-JUN-1998;	98US-091010P.
PR	01-JUL-1998;	98US-091359P.
PR	01-JUL-1998;	98US-091544P.
PR	02-JUL-1998;	98US-091478P.
PR	02-JUL-1998;	98US-091486P.
PR	02-JUL-1998;	98US-091626P.
PR	02-JUL-1998;	98US-091628P.
PR	02-JUL-1998;	98US-091632P.
PR	24-JUL-1998;	98US-094006P.
PR	04-AUG-1998;	98US-095282P.
PR	10-AUG-1998;	98US-095998P.
PR	10-AUG-1998;	98US-096012P.
PR	17-AUG-1998;	98US-096757P.
PR	17-AUG-1998;	98US-096766P.
PR	17-AUG-1998;	98US-096867P.
PR	17-AUG-1998;	98US-096897P.
PR	17-AUG-1998;	98US-096897P.
PR	18-AUG-1998;	98US-096949P.
PR	18-AUG-1998;	98US-096959P.
PR	18-AUG-1998;	98US-097022P.
PR	26-AUG-1998;	98US-097952P.
PR	26-AUG-1998;	98US-097954P.
PR	26-AUG-1998;	98US-097955P.
PR	26-AUG-1998;	98US-097971P.
PR	26-AUG-1998;	98US-097974P.
PR	26-AUG-1998;	98US-098014P.
PR	01-SEP-1998;	98US-098716P.
PR	01-SEP-1998;	98US-098723P.
PR	02-SEP-1998;	98US-098803P.
PR	02-SEP-1998;	98US-098821P.
PR	02-SEP-1998;	98US-098843P.
PR	09-SEP-1998;	98US-0989602P.
PR	10-SEP-1998;	98US-099741P.
PR	10-SEP-1998;	98US-099754P.
PR	10-SEP-1998;	98US-099763P.
PR	10-SEP-1998;	98US-099812P.

Alignment Scores:	
Pred. No.:	2,54e-153
Score:	2255.00
Percent Similarity:	74.92%
Best Local Similarity:	74.75%
Query Match:	83.70%
DB:	25
Length:	2764
Matches:	450
Conservative:	1
Mismatches:	3
Indels:	148
Gaps:	2

US-09-937-636-3 (1-512) x ABX97802 (1-2764)

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Db	46	ATGCTATCTGGCACTGGCTGGCTCTCGCTGGCGGGGATCCCAAGCATATGATGGAGA	105
QY	21	PhenTrIleArgValGlnGlnIuSerValMetVal1ProGlnGlyLeuCysIleSerValPro	40
Db	106	TTCTGGCATATGAGTATGAGAGTACAGATGATGGCGGAGGGCGCTGATCTCTGTCGCC	165
QY	41	CysSerPheSerIyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTTCTCTCAACCCCGACAGACTGGAAGGATCTACCCCAAGCTTATGGCTACGG	225
QY	61	PhenIysAlaValThrGlnThrThrTyrGlyAlaProValAlaThrAsnHisGlnSerArg	80
Db	226	TTCAAAAGCACTGACTGAGCAACCAAGGGTCTCTGTGGCGACAAACCAACAAGTCA	285
QY	81	GlnValGlnIuMetSerThrArgGlyArgPheGlnIleuTrpGlyAspProAlaIysGlyAsn	100
Db	286	GAGGTGAATATGAGCAACCCGGGGCCGATTTCCAGCTCACTGGGGATGCCGCCAAGGGGAAAC	345
QY	101	CysSerIeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPheArgVal	120
Db	346	TGCTCCCTTGATGTATGAGACCGGAGATGAGATGATGATGATCACTATCTTTTCGGGATG	405

QY	121	GIUA	rggISySeTtYyValArgrYrAsnPheMeTAsAspGlyPheHeuLySValThr	140
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KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
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PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07552.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
```


QY 41 CysSerPheSerThrProArgGlnAspTyrThrGlySerThrProAlaTyrGlyTyrTrp 60
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 Db 166 TGCTCTTCTCTACCCCGACACAGACTGGACAGGGCTTACCCAGCTTATGGCTACTGG 225
 QY 61 PheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
 |||||
 Db 226 TTCAAAGCAGTGTGACGACCAACCAAGGGGTCTCGTGGCCCAAAACCAACGACAGTGA 285
 QY 81 GluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyLysProAlaLysGlyAsn 100
 |||||
 Db 286 GAGGTGGAATGAGCACCCTGGGGCCGATTCACACTGAGGATCCCGCAAGGGGGAAC 345
 QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
 |||||
 Db 346 TGTCTCTGTGTATGACAGACGCGCAGATGACAGATGACACAGTACTCTTCTGGGGT 405
 QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
 |||||
 Db 406 GAGAGAGGAAGCTATGTGACATATTAATTCATGACAGATGGTCTTCTTAAAGTACAA 465
 QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
 |||||
 Db 465 ----- 465
 QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGluCysProProPheSerPheSerTrp 180
 |||||
 Db 465 ----- 465
 QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
 |||||
 Db 466 -----GTCCTC 471
 QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
 |||||
 Db 472 AGGTTACAGCCCGACAGCCCGACACACACGACCTCACCTGCGCATGGGACTTCTCC 531
 QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
 |||||
 Db 532 AGAAAGGCTGTGACGCGACAGAGAGACCGTCCGACTCCGTGGCTATGGCCCCAGAGAC 591
 QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
 |||||
 Db 592 CTGTATATCAGCATTTTCAGTACACACCGCAGCCCTGGAGCCCCAGCCCAAGGAAT 651
 QY 252 ----- 252
 Db 652 GTCCCATACCTGGAAGCCCAAAAGCCAGTTCCTGCGGCTCTGTGCTGCTGACAGC 711
 QY 252 ----- 252
 Db 712 CAGCCCCCTGCACACTGAGCTGGGTCTGCTGACAGACAGAGTCCCTCTGTCCTCATCC 771
 QY 252 ----- 252
 Db 772 TGGGGCCCTAGACCCTGGGGCTGAGAGCTGCCGGGTGAAGCTGGGATTCAGGGCGC 831
 QY 252 ----- 252
 Db 832 TACACCTGCGGAGGGAAGAGGCTTGGCTCCACAGCAGGAGCCCTGGAATCTCTGTG 891
 QY 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
 |||||
 Db 892 CAGATCTCTCCAGAGAACTGAGAGTATGTTTCCCAAGCAAAACAGACAGTCTGAA 951
 QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuCysLeuValCys 290
 |||||
 Db 952 AACCTTGGGAAGCGACAGTCTCTCCAGTACTGAGGGCCAAAGCCGTGCTGTGCTGT 1011
 QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
 |||||
 Db 1012 GTCACACAGACAGCCCGCCAGCGCTGAGTGGACCCAGAGGGGAGAGGTTCTGAGC 1071

QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnHisGln 330
 |||||
 Db 1072 CCTCCAGGCCCTCAGACACCCCGGGGGTCTGGAGCTGCTCGGTTCAAGTGGAGCAAGAA 1131
 QY 331 GlyGlnPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
 |||||
 Db 1132 GAGAGTTCACCTGCGCAGCGTCCGACCCCACTGGGCTCCAGCAGCTCTCTCAGCCCTC 1191
 QY 351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
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 Db 1192 TCCGTCCACTATTAAGAAAGGACATCTCAACGGCATTTCTCAACGAGCGTTCTGGGA 1251
 QY 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleLeuMetLysIleLeuPro 390
 |||||
 Db 1252 ATGGGATTCAGCGCTCTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
 QY 391 LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu 410
 |||||
 Db 1312 AAGAGACGCACTGACAGACAAACCCGAGGCCAGGTTCTCCCGCACACAGCATCTTG 1371
 QY 411 AspTyrIleAsnValAlaProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
 |||||
 Db 1372 GATTACATCATATGTGTCCCGACGGCTGGCCCTGGCTCTGAAAGCGGAATTCAGAAAGCC 1431
 QY 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlnSerLysLys 450
 |||||
 Db 1432 ACACCAAAACAGTCTCTCGAGACCCCTCCACACAGTGTCTCCCGCAGAAATCAAGAG 1491
 QY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGlnProLysSerSerThrGlnAla 470
 |||||
 Db 1492 AACCAAGAAAGCAGTATCAGTTGCCCCAGTTTCCAGAAACCAAAATCATCTCAAGGCC 1551
 QY 471 ProGlnSerGlnGlnSerGlnGlnGlnGlnHisTyrAlaThrLeuAsnPheProGlyVal 490
 |||||
 Db 1552 CCGAATCCCGAGAGAGCCCAAGAGAGACTCATTAATGACACGCTCAACTTCCAGAGCGTC 1611
 QY 491 ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
 |||||
 Db 1612 AGACCGAGGCTGAGGGCCCGGATGCCCAAGGGCCAGCGGATTTATGAGAAAGTCAAG 1671
 QY 511 PheGln 512
 |||||
 Db 1672 TTCCAA 1677

Search completed: October 8, 2003, 20:13:22
 Job time : 459 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:04:22 : Search time 3160 Seconds
(without alignments)
3937.940 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLLSLSLGGSGAMDGR.....RPEARMPKGTQADYAEVAFQ 512

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlh
-MODEL-frame.p2n.model -US09937636/runat_08102003_083236_29976/app-query.fasta.1.711
-DB-cgn2.1/USPPO/US09937636/runat_08102003_083236_29976/app-query.fasta.1.711
-DB-EST -QFMT-fastap -SUFFIX-p2n.ref -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITs-bits -START-1 -END-1 -MATRIX-biosum62 -TRANS-human4.0.cdi -LIST-45
-LOCALALIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-eto -NORM-ext -HEADSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09937636.ecgn.1.1.2810_etunat_08102003_083236_29976 -KCPU-6 -ICPU-3
-NO_MAP -LANGUEUSER -NEG SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOC
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_png:*
27: em_gss_vr1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1211.5	44.8	2017	11	AK042488 Mus muscu
2	1027.5	38.0	1201	13	BX345667 BX345667
3	1026.5	37.9	3939	11	AK036698 Mus muscu
4	927	34.3	1099	12	BM544297 BM544297
5	895.5	33.1	876	13	BO711946 BO711946
6	824.5	30.5	667	14	CB554607 CB554607
7	789	29.2	514	2	BSM097253 Bx470328 Homo sapi
8	734	27.1	1464	12	BM544269 BM544269
9	682.5	25.2	1060	12	BM925147 BM925147
10	669.5	24.7	2478	11	AK087658 AK087658
11	652	24.1	1745	12	BM906520 BM906520
12	629	23.2	995	12	BM922784 BM922784
13	621	22.9	1012	12	BM922958 BM922958
14	619.5	22.9	997	12	BM921873 BM921873
15	598.5	22.1	864	14	CB992313 CB992313
16	597.5	22.1	936	10	BF663289 BF663289
17	594.5	22.0	1201	13	BX399458 BX399458
18	591.5	21.9	830	12	B1906741 B1906741
19	587.5	21.7	1201	9	AL542696 AL542696
20	570.5	21.1	888	14	CA495365 CA495365
21	567.5	21.0	857	13	BO883649 BO883649
22	560.5	20.7	1191	9	AL542471 AL542471
23	556.5	20.6	916	12	B1910568 B1910568
24	550	20.3	1714	11	BC030222 BC030222
25	544	19.9	505	13	BX283650 BX283650
26	538.5	19.9	1121	12	BM564074 BM564074
27	538	19.9	871	12	B1518708 B1518708
28	534.5	19.8	2220	11	BC035688 BC035688
29	533.5	19.7	780	14	CB961761 CB961761
30	533	19.7	934	13	BX324896 BX324896
31	530.5	19.6	1001	12	BM561814 BM561814
32	530.5	19.6	1071	12	BM920861 BM920861
33	530	19.6	1793	11	AK046303 AK046303
34	514.5	19.0	1049	13	BO072659 BO072659
35	513	19.0	809	14	CB992745 CB992745
36	508.5	18.8	2378	11	AK089205 AK089205
37	493.5	18.2	1201	9	AL540764 AL540764
38	489	18.1	655	14	BY723555 BY723555
39	487.5	18.0	1397	9	AF150143 AF150143
40	486	18.0	1036	13	BO072894 BO072894
41	484.5	17.9	1201	13	BX345663 BX345663
42	479	17.7	795	12	B1822428 B1822428
43	468	17.3	510	12	BM483921 BM483921
44	463	17.1	706	12	B1911521 B1911521
45	459.5	17.0	1149	12	BM564076 BM564076

ALIGNMENTS

RESULT 1
AK042488
LOCUS
DEFINITION
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SLALC
ACID-BINDING LECTIN [Homo sapiens], full insert sequence.
ACCESSION
AK042488
VERSION
AK042488.1 GI:26335142
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

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AUTHORS

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

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Kono, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, T., Nakamura, S., Hazama, M., Nishino, T., Harada, S.,
Yamamoto, R., Matsumoto, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multipipillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I.,
Saito, T., Okazaki, Y., Gojodori, T., Bono, H., Kasukawa, T., Saito, R.,
Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nkaido, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Stubbli, F., Suzuki, R., Tomita, M.,
Wagner, R., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hotamoni, L., Hume, D. A., Kamuya, M., Lee, N. H., Lyons, P.,
Machlouni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P.,
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Functional annotation of a full-length mouse cDNA collection
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Group Phase I & II Team.
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Nature 420, 563-573 (2002)

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Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirose, T.,
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohtsuo, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Yamada, Y. M. and Hayashizaki, Y.

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AUTHORS

7 Direct Submission
Submitted (15-JUL-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for genome

JOURNAL

COMMENT	FEATURES	Source	CDS
<p>Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp), URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.</p> <p>Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.</p> <p>Please visit our web site for further details.</p> <p>URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/. Location/Qualifiers</p>	<p>1. 2017</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="FANTOM.DB:A630096C01"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="A630096C01"</p> <p>/tissue_type="thymus"</p> <p>/clone_id="RIKEN full-length enriched mouse cDNA library"</p> <p>/dev_stage="3 days neonate"</p> <p>147. >2015</p> <p>/note="unnamed protein product; putative weakly similar to STALIC ACID-BINDING LECTIN (Homo sapiens) (SPTR1Q96RL6, evidence: FASTY, 61.6%ID, 84.6%length, match=1719)"</p> <p>/codon_start=1</p> <p>/protein_id="BAC31272.1"</p> <p>/db_xref="GI:26335143"</p> <p>/translation="MSLLFLFLSLFDLPGQMESYFLQVRIKAQEGCLIFVPCSFSSPPEKQKNSPLGVGWFKGIRKSLSFPAVNNKKDLVEMEARGRFOLLGDISSKNC SLIKDKQMDSDFTNYPFRMGEPERFSEKCFIPQVATLQKPIFLIPELGEPEPT VCLLSTFTNQCPSRFSNMKDAVSFDESRHRTSNYSVLFIQLQHHDELTCQADF SRMSIOTVRILRAVAPRSLAISLIFHDNVSPDLNHPSHLEVOGSLYLCTADSQ PPAFLSWLEDOVLVMSWPVGSRTLALELPVKAKGSHYTCQAEENLGSQQLTDLIS VLYIPQDLRVYTSQANRTVLEILNNAISLPELSEQSCLVCVYSNPANVSNAMVQ TLIPDIQSEPEVLPLVPIQREHEGEFCAQNPPLGAQRISLSLVHPQMSSPSCSM EAKILHNCSSRRAMPARSLMRIRGEGLEGNSSAFTFESSLGPVWNSLSLLOEL GPSTWISCSNMTGAGQTTSTILLIPDDSAFASKGAVLGRGITALALLIIVYVT LQKGTQDEBRRLSLSGSTILLDITINYPKTRSLRANMKADPAPRSSPLDTHFR"</p>	<p>BASE COUNT 459 a 605 c 505 g 448 t</p> <p>ORIGIN</p>	<p>Alignment Scores:</p> <p>Pred. No.: 2,08e-91 Length: 2017</p> <p>Score: 1211.50 Matches: 270</p> <p>Percent Similarity: 51.92% Conservative: 55</p> <p>Best Local Similarity: 43.13% Mismatches: 114</p> <p>Query Match: 44.77% Indels: 188</p> <p>DB: 11 Gaps: 8</p>
US-09-937-636-3 (1-512) x AK042488 (1-2017)			
Qy 2 LeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetaspGlyAlaPhe 21			
Db 153 CTGCTGCGTGTCTCCGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAC 212			
Qy 22 TrpIleArgValGlnGlnUserValMetValProGlnGlyLeuGlySIIeserValProGly 41			
Db 213 TTCTTACAGGTGCAGAGATTGTGAAGGCACAGAGGGGTCTGTGCATCTTCTGTCCTTGC 272			
Qy 42 SerPheSerTyrProAlaGlnAspTrpPheGlnGlySerThrProAlaTyrGlyTyrTrpPhe 61			
Db 273 TCTCTTCTCTCCCTGAGGAAATGGCTTAACGGTTCCTCCACATTATAGCTACTGGTTC 332			
Qy 62 LysAlaValThrGlnThrThrLysGlyValAlaProValAlaThrAsnHisGlnSerArgGln 81			

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Db      333 AAAGCATGAAAAACCATCTTTCATTTCCAGTGGCCACAAATAACAAAGATAAGTG 392
Qy      82 ValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyLys 101
Db      393 TTAGATGGGAAAGCCCGGAGGGCTTCCAGCTTGGGGATATCTCAAAAAGAACTGT 452
Qy      102 SerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnIleThrPheArgValGlu 121
Db      453 TCCTTGCTAATCAAGATGTTTCAGTGGGAGAGCTCAACAACCTATTCTTCGGATGGAG 512
Qy      122 ArgGlySerThrValArgIleAspPheMetLysAspGlyPhePheLeuLysValThrAla 141
Db      513 AGAGGA---TTGAGAGATTCAGTTTCAAGAGAGG---TTCAGGCTCAAGTGAAGCC 566
Qy      142 LeuThrGlnLysProAspValIleProGluThrLeuGluProGlyGlnProValThr 161
Db      567 CTGACTCAGAAAGCCAGATATCTTCATCTCTGAGTCTGAGGCTGAGGAGCCAGCTGACC 626
Qy      162 ValIleCysValPheAsnThrAlaPheGlnGluCysProProSerPheSerThrThr 181
Db      627 GTTGCTGCTGTTTTCCTGGACCTTCAACCAATGCCAGCTCTTCTTCTCCGTGATG 686
Qy      182 GluAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeuSer 201
Db      687 GGGAGTGGCTGCTCTCCCAAGAAAGCAGACCCGACATCCCAATTACATCTGTGAGC 746
Qy      202 PheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSerArg 221
Db      747 TTTATCCCAAGACTTCAACACCATGTACTGAGTGCACATGTACACTTCTCTAGA 806
Qy      222 LysGlyValSerAlaGlnArgThrValArgLeuArgValAlaIleValAlaProArgLysLeu 241
Db      807 -----ATGAGACACAAAGACCTGCTCGACTTAAGAGTGGCTATGCCCCAGATCTCT 860
Qy      242 ValIleSerIleSerArgAspAsn-----ThrProAsp----- 252
Db      861 GCTATCAGACATTTTCCATGACAAATGTATACGCCAGACTTCGAGAAATCCTACAT 920
Qy      252 ----- 252
Db      921 CTGGAAGTTCAAGCAAGCCAGTCTCTGCTCTGTACTGATGTCGACAGCCGCCCT 980
Qy      252 ----- 252
Db      981 GCTACACTGAGCTGGGCTCTAGAGACCAAGTCTTTCTTGCTAGCCCTGTGGGCTGC 1040
Qy      252 ----- 252
Db      1041 AGAACCCCTGGCAGTGAAGTGGCTGGGTAAGAGTGGGAGACTTGGACACTACACTTGC 1100
Qy      253 -----Pro 253
Db      1101 CAAGCAGAGAAATAGGCTGGCTCCCAAGCAACATACCTCGACCTCTGTGCTGTAACCC 1160
Qy      254 ProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlnLysLeuGly 273
Db      1161 CCACAGGACCTGAGAGTACTGTTCCCAAGCAACAGACAGTGTGTGAAATCTCTCAGG 1220
Qy      274 AsnGlyThrSerLeuProValLeuGlnLysIleSerLeuCysLysLeuValCysValThrHis 293
Db      1221 AATGCCATCTCCCTCCAGTCTCTGAGAGGCCAAAGCCTGTGCTAGTGTGCTACATAT 1280
Qy      294 SerSerProProAlaArgLeuSerThrThrGlnArgGlyGlnValLeuSerProSerGln 313
Db      1281 AGCAATCCCGCCCAATGTGAGTGGCTTGGGTGACACAGACCTCATCCCAATCCAG 1340
Qy      314 ProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnHisGlnGluLysPhe 333
Db      1341 TCTTGAAGACCTGGGGTCTCTGAGCTGCTCTGCTGTCACAGACAAATGAGAAATTC 1400
Qy      334 ThrCysHisAlaArgHisProLeuGlnLysSerGlnHisValSerLeuSerLeuSerValHis 353

```

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Db      1401 ACCTGTGCTGCACAGAACCCACTGGGTGCCAGCGCATCTGTGAGCCCTCTGTGCAC 1460
Qy      354 Tyr-----LysGlyLeu----- 358
Db      1461 TACCCGCCCAAGATGTCAGGCCCTCTCTCTCTGGAGGCCAAGGTCCTGACTGCACAC 1520
Qy      358 ----- 358
Db      1521 TGTCTCTCAGAGCTGGCCCTGCCCCCTTCCTGCGCTGCGGCTGGGGAGGGGCTGCTG 1580
Qy      358 ----- 358
Db      1581 GAGGGGAACAGACGATGCTCTCTCAAGTCACTTCAAGTCACTTGAACCTGGGTC 1640
Qy      358 ----- 358
Db      1641 AACAGCTCCCTGAGCTCTCTCAGAGGCTGGGGCCAGCCCTGTGCTGAGTGTCC 1700
Qy      359 -----LysSer 360
Db      1701 TGGAAACACCATGAGGCCCAAGACACCTGTCTGCTGCTACCTGATTAAGACAGTGC 1760
Qy      361 ThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuPheLeuGly 380
Db      1761 ACAGCATCTCCAAAGGAGAGAGTGTGGGCTTGGCATACAGACCCCTGCTGCTGTC 1820
Qy      381 LeuAlaLeuIleIleMetLysIleLeuProLysArgValThrGlnThrGluThrProArg 400
Db      1821 CTCATCTGCTGCTATGTGTAAAGACCTCCAGAAAGAAAGAACCCAGAGGAACCTCCAGG 1880
Qy      401 ProArgPheSerArgHisSerThrIleLeuAspThrIleAsnValProThrAlaGly 420
Db      1881 CCCAAGCTCTCCGGGAGAGCAGATCTGGGCTGATCATCATCAATGTGTCCTCCAGACGAG 1940
Qy      421 ProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440
Db      1941 TCCCTGGCT-----CGGAATGGAAAGATGAACAGATGCCCTTCTAG-GAGCTACCC 1993
Qy      441 ProGlyAlaProSerPro 446
Db      1994 CCTGCACTCACTTCCC 2011

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RESULT 2
 LOCUS BX345667 1201 bp mRNA linear EST 05-MAY-2003
 DEFINITION BX345667 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
 clone CS01025YC24 5-PRIME, mRNA sequence.
 ACCESSION BX345667
 VERSION BX345667.1 GI:30373021
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 invitrogen. This sequence belongs to sequence cluster 9384.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0A1025B120P1cluster-9384.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ invitrogen corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0A1025B120P1.
 Location/Qualifiers
 1..1201
 FEATURES
 source

[illegible][illegible]

Db 1113 AACATATATCATGATAGATTCATGATCTTGTATATAATGAGCAAGTTGCTGGGGAG 1172
QY 236 -----
Db 1173 ATGAGTAGCTGATTAAGAGTTTGACACACAGCCAGCGGGTGTGCACACCTTAGTC 1232
QY 236 -----
Db 1233 CCAACACTTGGGAGGAAGAGGCAAGCCGAATTTCTGAGTTTGAGGCCATCCTGCTACAG 1292
QY 236 -----
Db 1293 AGTGAGTGCAGGTCAAGCCAGGGGTACACAGAGAAACCTGTCTCAAAAAAAAAAAAAA 1352
QY 236 -----
Db 1353 AAAAAAAAAAAGAGTTTGACACACAGAGTGTGAGAAATGGATTTGAACCTCAGAGC 1412
QY 236 -----
Db 1413 ATGCATTAAGCCAGTCAGGCATGTAGCCCCACTGTAACCTCATCATCTTTGGAGACA 1472
QY 236 -----
Db 1473 GAGCAAGTAGTCCCAAGGCAAGTAGTAGCTAGAGCTGCTACCCATTAGCAAGCTC 1532
QY 236 -----
Db 1533 TGAGTTCMAATGAAGACCTGCCTCCTTAACAATGTAGACAGTAGATTGAGAGTAGCC 1592
QY 236 -----
Db 1593 TGGCTCCCCACACACTTATGTGCACATGTGTGCATCCATACACACATGCGATGCACA 1652
QY 236 -----
Db 1653 CATACATTTCAAAATCAAGCGAGAGGACACACCATCCGGGTGTGCCTAGCCGTGAGA 1712
QY 236 -----
Db 1713 GGGAGNGTTGCTTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTC 1772
QY 236 -----
Db 1773 TTTCCCTGAGGACTTCTCATGAGAACAAAGCATTCCTCGAAGTTGGCTCACAAT 1832
QY 237 -----
Db 1833 CTTCCTCCAGATGCCCCAGATCTCTGTATCAGCATTTTCCATGACATGT-ATCAGG 1891
QY 250 -----
Db 1892 TACGTGTGTCTCTGAGGCTTATAGGGCGGTCCATTCTTTTGGAAATGAAAAGTC 1951
QY 250 -----
Db 1952 TGGGGAAGGGGGAAGGGGAGGTTGAACTTTTACTGCTTCTCCCTACCCCTCATCT 2011
QY 250 -----
Db 2012 TGGTCCCTCTCCCTTCTCTTATGTCTGTCTGTGCCCCCTTATCTATCTTATAGCCT 2071
QY 250 -----
Db 2072 CTGTCTGTCTGTCTGTGTGTATGATTTTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2131
QY 250 -----
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QY 250 -----

Db 2192 TCTCATTTTGTCTGTCT 2251
QY 251 -----
Db 2252 CTCTCTGCGGTGTGTCT 2311
QY 252 -----
Db 2312 GTTCACCAAGGCCAGTCTCTTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2371
QY 252 -----
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QY 252 -----
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QY 253 -----
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QY 256 -----
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QY 276 -----
Db 2612 ATCTCCCTCCAGTCTCTGAGGGCCAAAGCCTTGCTTACTGTCTGTCTGTCTGTCTGTCT 2671
QY 2672 -----
Db 2672 CCCCAGCCAAATGATGATGTTGGCTGGGTGACACAGACCTGATCCAAATCCAGTCTCA 2731
QY 316 -----
Db 2732 GAGCCTGGGTCTGTGAGCTGCTCTGTCTGACAGAAATCAAGAGATTCACCTGT 2791
QY 336 -----
Db 2792 GCTGCACAGAACCATCTGGTGGCCAGCGCATCTCTGTGAGCCTCTGTGTGACCTGTGAG 2851
QY 355 -----
Db 2852 TAGCAAAAGGACACTGGGATCTGTGATGAGGGCCAGCTGCTGACATTTCTCTCTC 2911
QY 356 -----
Db 2912 CACAGACCGCCAGATGTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2971
QY 357 -----
Db 2972 CAACCTGCTCTCAGAGCTGGGCTGCCCTGCCCTGCGCTGGCGGCTGGGGAGGGGCT 3031
QY 358 -----
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QY 359 -----
Db 3092 GGTCAACAGCTCCCTGAGCCTCTCTCAGAGCTGGGGCCAGCCTCTGGCTCAGCTGTGA 3151
QY 359 -----
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QY 360 -----
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QY 379 -----
Db 379 -----
Db 3272 GTGCTCTCATCTGTGTATCTGTGAAGACCTCTCAGAAAGAAAGAACCCAGAGGAGACCTC 3331


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QY      312 --SerGlnPro-SerAspPro-----GlyValLeuGluLeuPro 323
Db      894 TCCACGCCCTGGGGGATCCCCCTAAACCCCTTGGGGCCACTTAACCTTACTCTGCATACCA 953
QY      324 ArgValGlnValGluHis-----GluGlyGlu 332
Db      954 AAATGTTTCTGGCGCCATTATTCGGCCTTCATTAACACACTCCCAACATGCTCTCAAGCT 1013
QY      333 PheThrCysHisAlaArgHisPro 340
Db      1014 CACAGCTGCTATCATATATACCT 1037

RESULT 5
B0711946
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B0711946      876 bp      mRNA      linear      EST 16-JUL-2002
AGENCOURT_7977108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215765
5', mRNA sequence.
B0711946
B0711946.1 GI:21850845
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 876)
NIH-MGC http://mgs.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM2385 row: d column: 06
High quality sequence stop: 685.
Location/Qualifiers
1..876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6215765"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
BASE COUNT      176 a      304 c      244 g      151 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      2 97e-65      Length:      876
Score:      895.50      Matches:      190
Percent Similarity:      65.19%      Conservative:      1
Best Local Similarity:      64.85%      Mismatches:      4
Query Match:      33.09%      Indels:      98
DB:      13      Gaps:      1

US-09-937-636-3 (1-512) x B0711946 (1-876)
QY      260 MetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuPro 279
Db      2 ATGGTTTCCCAAGCAAGACAGACAGCTCGGAAACCTTGGGCAACGCACTCTCCCA 61
QY      280 ValLeuGluGlyGlnSerLeuValCysValThrHisSerProProAlaArg 299

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Db      62 GTACTGAGGAGCCAAAGCCTGTGCTGTGTCTGCACACAGACAGCCCCCAGCCAGG 121
QY      300 LeuSerTrpPheGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyVal 319
Db      122 CTGAGCTGAGACCCAGAGGGGACAGGTTCTAGCCCCCTCCAGCCCTAGACCCCGGGGTC 181
QY      320 LeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHis 339
Db      182 CTGAGCTGCTCGGGGTTCAAGTGAGCAGCAGGAAGAGTTCACTGACCTCCAGCTGGCAGC 241
QY      340 ProLeuGlySerGlnHisValSerLeuSerLeuSerValHisTyr----- 354
Db      242 CCACTGGCTCCAGCAGCAGTCTCTCTAGCTCTCGTGACACTCTCCCGAAGCTGCTG 301
QY      354 ----- 354
Db      302 GGCCCTCTCTGCTCTGGAGGCTGAGAGGTCTGCACACTGCAGCTCTCTCCAGGCCAGC 361
QY      354 ----- 354
Db      362 CCGGCCCTCTCTGCTGCTGTGTGGGAGAGCTGCTGGAGGGGAACAGCAGCAG 421
QY      354 ----- 354
Db      422 GACTCTTGAGGTACACCCCACTGACGCCGGGCGCTGGGCAACAGCTCTGAGCTTC 481
QY      354 ----- 354
Db      482 CATGAGAGGCTCAGCTCCGGCTCAGGCTCCGCTGTGAGGCTGGAACGTCTATGGGGCC 541
QY      355 ----- 355
Db      542 CAGAGTGATCCATCTCTGAGCTGCAGATTAAGAAAGGAGCTCATTCACAGGATTCCTCC 601
QY      365 AsnGlyAlaPheLeuGlyIleGlyIlePheAlaLeuPheLeuCysLeuAlaLeuIle 384
Db      602 AAGGAGCGCTTCTGGGATCGGCATCAGCGCTCTCTTCTCTGCTGCGCTGCGCTGATC 661
QY      385 IleMetLysIleLeuProLysArgArgThrGlnThrGluThrProArgProArgPheSer 404
Db      662 ATCATGATGATCTTACCGAAGAGCAGCTCAGACAGAAACCCCGAGGCTCTCTCC 721
QY      405 ArgHisSerThrIleLeuAspTyrIleAsnValValProThrAlaGlyProLeuAlaGln 424
Db      722 CGGCACAGACGATCTTGATTTACATCAATGTGGTCCGACGGCTGGCCCTGGGCTCAG 781
QY      425 LysArgAsnGlnLysAlaThrProAsnSerPro-ArgThrProLeuProGlyAla-- 443
Db      782 AAGCGAATCAAAAAGCCACACCAAAACAGTCTTGGAGCCCTTCACAAAGGTGGCTC 841
QY      444 ProSerProGluSerLysLysAsnGlnLysLys 454
Db      842 CCNTCCCGGAATCCAAAGAGAACCCGCAAAA 874

RESULT 6
CB554607
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB554607      667 bp      mRNA      linear      EST 01-JUN-2003
MMSF0040_D05 MMSF Macaca mulatta cDNA, mRNA sequence.
CB554607
CB554607.1 GI:31303802
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 667)
Katz, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
Expressed sequence tags from Rhesus macaque spleen
Unpublished
Contact: Holzman T

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QY 81 GluValGluMetSerThrArgGlyArgPheGluLeuThrGlyAspProAlaIysGlyAsn 100
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 Db 303 GAGGTGAAATGAGACACCCGGCCGATTCACGCTCTGCGGATCCCGCCAGGGAGAC 362
 QY 101 CysSerLeuValIleArgAspAlaGluMetGlnAspGluSerGlnIlyPhePheArgVal 120
 |||
 Db 363 TGCCTCTGGTGTATCAGACAGCGCAGATGACAGATGATGACAGTACTCTTCCGGGTG 422
 QY 121 GluArgGlySerIlyValArgIlyAsnPheMetAsnAspGlyPhePheLeuIlyValThr 140
 |||
 Db 423 GAGGAGGAGAGCATGTAGATATAATTCATGAACGATGGTCTTTAAAGTAAACA 482
 QY 141 AlaLeuThrGlnIlyProAspValIlyIle 150
 |||
 Db 483 GCCCTGACTCAGAAAGCCTGATGCTACATC 512

RESULT 8
 BM544269 1464 bp mRNA linear EST 20-FEB-2002
 LOCUS AGENCOURT_6490879 NIH_MGC_125 Homo sapiens cDNA IMAGE:5587773
 DEFINITION 5', mRNA sequence.
 ACCESSION BM544269
 VERSION BM544269.1 GI:18775382
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1464)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M12357 row: m column: 22
 High quality sequence start: 87
 High quality sequence stop: 427.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5587773"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_125"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
 Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
 of three ovaries, from females ranging in age from 38 to
 49 yo. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb, insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research genetics
 tracking code 036."
 BASE COUNT 296 a 545 c 267 g 352 t 4 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,29e-51 Length: 1464
 Score: 734.00 Matches: 209
 Percent Similarity: 44.97% Conservative: 37
 Best Local Similarity: 38.21% Mismatches: 131
 Query Match: 27,128 Indels: 171
 12 Gaps: 16

US-09-937-636-3 (1-512) x BM544269 (1-1464)
 QY 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyIlySerGlnAlaMetAspGlyArg 20
 :|||
 Db 99 CTGCTGCTGCCCTGCTGCTGCCGCTGCTGCGGGGGGGGCTCCGTGAACAATGATCCAGT 158
 QY 21 PheTrpIleArgValGlnGlnSerValMetValProGluIlyLeuCysIleSerValPro 40
 :|||
 Db 159 TACAGCTTCAAGTCGACGAGGACGAGTCCGCTGCGGAGGCGCTGTGTGATCGTGTCT 218
 QY 41 CysSerPheSerIlyProArgGlnAspTrpThrGlySerThrProAlaIlyGlyIlyTrp 60
 :|||
 Db 219 TGCACCTCTCTACACCCCGGAGTGGCTGGAGCAGCTACCTGCTGTGTGCTACTGG 278
 QY 61 PheIlyAlaValThrGluThrIlyGlyAlaProValAlaThrAsnIlyGlnSerArg 80
 :|||
 Db 279 TTCAAAGGACGAGACACCCCAAGACGGGTCTCTGTGACATCAACACAGAGTGA 338
 QY 81 GluValGluMetSerThrArgGlyArgPheGluLeuThrGlyAspProAlaIysGlyAsn 100
 :|||
 Db 339 GAGGTGCAATGAGACACCCGGACCCGATTCACGCTCTGAGTCCCGGCAAGGAGAC 398
 QY 101 CysSerLeuValIleArgAspAlaGluMetGlnAspGluSerGlnIlyPhePheArgVal 120
 :|||
 Db 399 TGCCTCTGGTGTATCAGACAGCGCAGTGGAGAGATGAGCATGTACTCTTCCGGGTG 458
 QY 121 GluArgGlySerIlyValArgIlyAsnPheMetAsnAspGlyPhePheLeuIlyValThr 140
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 Db 459 GAGAGAGGAGAGCGCGGAGACATAGTTATAGCAATCGTTCTTTCAAAAGTAAACA 518
 QY 141 AlaLeuThrGlnIlyProAspValIlyIleProGluThrLeuGluIlyProGluIlyGlnProVal 160
 :|||
 Db 519 GCCCTGACTCAGAAAGCCTGATGCTATGATCCCGAGACCCCTGAGCGCGGTGCGGGG 578
 QY 161 ThrValIleCysValPheAsnTrpAlaPheGluGlyCysProProSerPheSerTrp 180
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 Db 579 ACGGTATGCTGTGTGTTCACTGCGGCTTCACAAATGTCACCCCTTCTCTCTCTG 638
 QY 181 ThrGluAlaLeuSerSerGlnGlyThrIlyProThrIlySerHis-----Phe 197
 :|||
 Db 639 ACGGGGCTGCT 692
 QY 198 SerValLeuSer-PheThrProArg-ProGlnAspHisAspThrAspLeuThrCysHisIly 217
 :|||
 Db 693 TCCCTGCTGACCTTCACGCCCAACCCCGAGACAC----- 730
 QY 217 AlaPheSerArgIlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaIlyArg 237
 :|||
 Db 730 ----- 730
 QY 237 LeuProArgAspLeuValIleSerIleSerArgAspAsnThrProAspProProGluAsnL 257
 :|||
 Db 730 ----- 730
 QY 257 euArgValMetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyHis 277
 :|||
 Db 731 -----GGAACCGAACCTTC-----A 746
 QY 277 etLeuProValLeuGluGluGlnSerLeuCysLeuValIlyThrHisSerSerPro 297
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 Db 747 CCTGTGCCATG-----GTGGGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 775
 QY 297 roAlaArgLeuSerTrpThrGlnArgGlyGluValLeuSerProSerGlnProSerAspR 317
 :|||
 Db 776 -----AAAAGGGT-----GTGTGCAACCTTCACCTATAGGCAAC 812
 QY 317 roGlyValLeuGluLeuProArgValGlnVal-----GluHisG 330
 :|||
 Db 813 CAGCTCTCTGACACCTCCCGGGGTGGTCCCTCCCTCATGTAGTAATCTCCSSAC 872
 QY 330 IuGlyGluPheThrCysHisAlaArg-----H 339
 :|||
 Db 873 ATGGCCCAAAATCCCTCACTTAACACACTTACCTTGGGCCCAAAATTTTTCCTATCC 932

Oy		339	ISPRoleunglySerClnHIsValSerleuSerleuServalHisTylLyslysGlyLeuI	359
Db		933	 ACCCCATATCCGGTTTCCACCAGCTTATTCC-----	964
Oy		359	IeSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeu-----	377
Db		965	-----TCCTTAAGCCCGTTGGCCCCCTATCGCCTTATCCCCTTTCTGTACC ::: 965	1010
Oy		378	----PheLeuCysLeuAlaLeuIleMetLysileLeuProLysArgArghThriInt :: 378	396
Db		1011	CCTTTTTCATTGTGTTCAACTGCCCTATMAAAAGTCGTTAACACAAGATGCATCCA :: 1011	1070
Oy		396	hrgIutrrPro-----ArgProAargPheSerArghHiserThri 396	409
Db		1071	CACATACACCGGTTTATATACCCCTTTTGCGCTCACCCGATTCGAC-----AGTCAA 1071	1124
Oy		409	IeLeuAspTyrlIeAsnValValrProThrAlaglyProLeuAlaGlnIeAsnGngInl 409	429
Db		1125	TTCGCT-----CTTAACACCG 1125	1139
Oy		429	ySalatrrProAsnSerProArghThrProleuProProglyAlaPro----- 429	444
Db		1140	ACACACACACCTAAATGGCGACACCNCGCCCTATTCCTTATCCCTTCCTATAACA 1140	1199
Oy		445	-----SerProgluSerLyLysAsnGlnLysysG 445	455
Db		1200	CTCATTTGATATACACACCCCAACATACTTCCCTGGGTCNTTCCGCCCTAACCTCC 1200	1259
Oy		455	InTrygInleuProSerPheProgluProLysSerSerThrGlnAlaProgluSerIng :: 455	475
Db		1260	GTAATTAACCGCCATTCCTCACACCCCGGATTAATAATAC-ACGCTGCCCCCAAAATACAC 1260	1318
Oy		475	IuSerGIngluGlnHistyralaThrIeAsnPrheProglyValArghProArghProg 475	495
Db		1319	CTCTCC-----CANCCTGTATTTCCCCACACCCCC 1319	1348
Oy		495	IuAlaArgMetProLys 500 495	500
Db		1349	CCATTTTTTATCCGCGT 1365 1349	1365
RESULT 9				
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LOCUS			BM925147	
DEFINITION			AGENCOURT 5627330 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762452	
ACCESSION			5', mRNA sequence.	
VERSION			BM925147	
KEYWORDS			BM925147.1 GI:19375526	
SOURCE			EST.	
ORGANISM			Homo sapiens (human)	
			Homo sapiens	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE			1 (bases 1 to 1060)	
AUTHORS			NIH-MGC http://mgc.nci.nih.gov/.	
TITLE			National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL			Unpublished	
COMMENT			Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnl.gov Plate: LHAM12812 row: 1 column: 05 High quality sequence stop: 725. Location/Qualifiers 1..1060 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	
FEATURES				
source				

[illegible]

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbsfemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: L1AM12795 row: K column: 02
High quality sequence stop: 637.
Location/Qualifiers

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BASE COUNT 220 a 320 c 268 g 187 t
ORIGIN

Alignment Scores:

Pred. No.: 9.76e-43 Length: 995
Score: 629.00 Matches: 156
Percent Similarity: 58.45% Conservative: 48
Best Local Similarity: 44.70% Mismatches: 115
Query Match: 23.24% Indels: 30
DB: 12 Gaps: 7

US-09-937-636-3 (1-512) x BM922784 (1-995)

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ACCESSION BM922958
VERSION BM922958.1 GI:19373337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 1012)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbsfemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: L1AM12798 row: d column: 15
High quality sequence stop: 609.
Location/Qualifiers
1. 1012
/organism="Homo sapiens"


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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2003, 20:04:52 ; Search time 93 Seconds

(without alignments)
2429.980 Million cell updates/sec

Title: US-09-937-636-3

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Ygapop 10.0, Ygapext 0.5
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%

Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	888	32.8	2900	3 US-09-038-832-1	Sequence 1, Appl1
3	831.5	30.7	1501	3 US-09-046-736-1	Sequence 3, Appl1
4	573	21.2	1502	3 US-09-046-736-3	Sequence 3, Appl1
5	528.5	19.5	1488	4 US-09-620-312D-407	Sequence 407, App
6	192	7.1	1339	3 US-08-468-856B-3	Sequence 3, Appl1
7	192	7.1	1339	3 US-08-468-859A-3	Sequence 3, Appl1
8	187	6.9	1630	3 US-08-468-856B-2	Sequence 2, Appl1
9	187	6.9	1630	3 US-08-468-859A-2	Sequence 2, Appl1
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20	156	5.8	2458	4 US-09-996-243-502	Sequence 502, App
21	152	5.6	4078	4 US-09-016-434-1120	Sequence 1120, App
22	151.5	5.6	4285	3 US-09-040-774-1	Sequence 1, Appl1
23	151.5	5.6	6814	4 US-09-484-970B-66	Sequence 66, Appl1
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45	138	5.1	1693	6 5169835-3	Patent No. 5169835

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09038832
; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIRKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Stalodhesin Family Member-2
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038.832
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

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RESULT 5

US-09-620-312D-407
 Sequence 407, Application US/09620312D
 Patent No. 6569662
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Tang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundang
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620, 312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552, 317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488, 725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: Pf-Fl.genes Version 1.0
 SEQ ID NO 407
 LENGTH: 1488
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (146)..(931)
 US-09-620-312D-407

Alignment Scores:

Pred. No.: 1,8e-41 Length: 1488
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US-09-937-636-3 (1-512) x US-09-620-312D-407 (1-1488)

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 Db 662 CTCACGATCATCCACGCGCTCAGGACCGAGGACCAACCTCATCTCAGGTGACGTTC 721
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 QY 281 ---LeuGlnIlyGlnSerLeuCysLeu-----ValCysValThrHis 293
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Db      1186  -----CTGAAATGGCCTTCTCCCAATTCCTGGCAATCCAGGT 1223
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Oy      382  AleuIleIleMet 386
Db      1284  TTGTATGATATATTA 1296

RESULT 6
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Sequence 3, Application US/08468856B
Patent No. 6013772
GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Eling, James; Kamarc, Michael;
APPLICANT: Kretschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 2.0 MB storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WordPerfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,856B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,678
FILING DATE: 16-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/060,031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: M01 242.10-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700

```

TELEFX: (914) 332-1844				
INFORMATION FOR SEQ ID NO: 3:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 1339 nucleotides				
TYPE: nucleic acid				
STRANDEDNESS: single				
TOPOLOGY: linear				
US-08-468-856B-3				
Alignment Scores:				
Pred. No.:	5,45e-09	Length:	1339	
Score:	192.00	Matches:	120	
Percent Similarity:	34.99%	Conservative:	70	
Best Local Similarity:	22.10%	Mismatches:	170	
Query Match:	7.10%	Indels:	183	
DB:	3	Gaps:	27	
US-09-937-636-3 (1-512) x US-08-468-856B-3 (1-1339)				
QY	5	LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyAArgPheThrPileArg	24	
Db	127	CTGCTCAGACCCCTTCTCTA-----ACCTTCTGGAAACCG	162	
QY	25	ValGlnGlnSerValMetValProGlnGlyLeuGlyIleSerValPro-----	40	
Db	163	CCGACCACTGCCAGCTCAGCTACTGAAATCCATTCATTCAAGTTGACGAGGGAAGAG	222	
QY	41	-----CysSerPheSerTyrrProArgGlnAspTrpThrGlySerThrProAlaTy	57	
Db	223	GTTCTTCTCTCTTCTCCACATCTGCCCCACGAA-----CTTTT	261	
QY	58	GlyTyrr--TrpPheIysAlaValThrGlnThrLysGlyAlaProValAlaThrAsn	76	
Db	262	GGCTGACAGCGCTACAAAGG-----GAAGAGTGATGCG-----	297	
QY	77	HisGlnSerArgGlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAsp	96	
Db	298	-----AACCGTAAATTTAGAGATTTGCATATGGAATCAACAAGCTTACCCAGGGCCC	351	
QY	97	AlaIysGly-----AsnGlySerLeuValIleArgAspAlaGln	109	
Db	352	GCAACAGCGGTGGAGAGACATATATACCCCATTCATCCCTGTGATTCACAAAGCTAC	411	
QY	110	MetGlnAspGlnSerGlnTyrrPhePheArgValGlnArgGlySerTyrrValArgTyrrAsn	129	
Db	412	CAGAAATGACAGAGATTCTACACCCATCAAGTC-----ATAAGTCAGAT	456	
QY	130	PheMetCAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyrr	149	
Db	457	CTTGTTGATGAA-----GAAGCAACCTGGACACTTCATGTTATAC	495	
QY	150	IleProGlnThrLeuGlnProGlyGlnProValThrValIleCysValIlePheAsnTrpAla	169	
Db	495	-----	495	
QY	170	PheGlnGlnCysProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly	189	
Db	496	---CCGAGAGTGGCCAAAGCCCTCC-----ATCTCCAGCAACAAC	531	
QY	190	ThrLysProThrThrSerThrIleSerValIleSerPheThrProArgProGlnAspHis	209	
Db	532	TCCAAACCTCTGGAGACAAGAGATGCTG---GCCCTTCACTCTGAACCTGAGACCTCAG	588	
QY	210	AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr	229	
Db	589	GACACCAACCTACTGTGGTGGATTAACAATCAGACCTCCCGGTAGTACC-----	639	
QY	230	ValArgLeuArgValAlaTyrrAlaProArgAspLeu--ValIleSerIleSerArgAsp	248	
Db	640	---AGCGTCAGCTGTCAATAGGCAACAGACCTCTACCTCAGTCAAGTCAACAAGAT	696	
QY	249	AsnThrProAspProProGlnLysLeuValMetValSerGlnAlaAsnArgThr---	267	

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Db      697 GACACAGAGCCCTATGATGTGAATAACAGAACCCAGTAGT---GGCAACCGCAGTGCAC 753
Qy      268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu-----282
Db      754 CCACTACACCTTGAAATGTACCTATATGGCCGAGACACCCACCACTATTTCCCTTCAGACACC 813
Qy      283 -----GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla 298
Db      814 TATTAACCGTCACAGGGGCAACACCTCAGCCTCTCTGATATGACAGCCTTAACCCACCTGCA 873
Qy      299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
Db      874 CAGTACCTCTGGCTTATCAATGAAACATTCACGCAAAACACACAGAG-----921
Qy      319 ValLeuGluLeuProArgValGlnValGlnHisGlnGlyGlnPheThrCysHisAlaArg 338
Db      922 ---CTCTTATTCCTTACATACATGATGATATATAGTGGATCTTATACCTGCACGCCCAT 978
Qy      339 HisProLeu---GlySerGlnHisValSerLeuSerValHisTyrLeuLysGly 357
Db      979 AACTCAGTCACTGGCTGCACACAGACACAGACATCAAGACATCAATGACACGATATATGCT 1038
Qy      358 Leu---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyIleThr 374
Db      1039 CTACCACAGAAATAATGGCTCTCTACCTGGGCGCATTTGCTGATGATGATGAGTAGTG 1098
Qy      375 AlaLeuLeu---PheLeuCysLeuAlaLeuIle-IleMetLysIleLeuProLysArgAr 393
Db      1099 GCCCTGCTCTCTGATACAGATGACCTGCGCATGTTTCTGCAT-----1144
Qy      393 GThGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrI1 413
Db      1145 -----TCGGGAAGACCGGAGCTCAGACACATCCCAT-----1177
Qy      413 eAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAs 433
Db      1177 -----1177
Qy      433 nSerProArgThrProLeuProProGlyAlaProSerProGluSerLysAsnGlnLys 453
Db      1178 -----GACCCACCTAACAGATGAT-----1198
Qy      453 sLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSe 473
Db      1198 -----1198
Qy      473 rGlnGlnSerGlnGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlyValArgPro-- 492
Db      1199 -----GAAATTACTTATTTCTACCTGAACTTGAAGCCGACAGCCAC 1242
Qy      493 -ArgProGluAlaArgMetProLys-----GlyThrGlnAlaAspTyrAlaGlnValLys 510
Db      1243 ACAACCAACTTACACCTCCCATCCCTAACAGCCACAGAAATATTTATTCAGAAAGTAA 1302
Qy      510 sPheGln 512
Db      1303 AAAGCAG 1309

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; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468, 859A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027, 974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760, 031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274, 107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207, 678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060, 031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016, 683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896, 361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1339 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-468-859A-3
; Alignment Scores:
; Pred. No.: 5.45e-09 Length: 1339
; Score: 192.00 Matches: 120
; Percent Similarity: 34.99% Conservative: 70
; Best Local Similarity: 22.10% Mismatches: 170
; Query Match: 7.10% Indels: 183
; Gaps: 27
; US-09-937-636-3 (1-512) x US-08-468-859A-3 (1-1339)
Qy      5 LeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrIleArg 24
Db      127 CTGCTCAGAGCTTACTTCTTA-----ACCTTCTGGAACCG 162
Qy      25 ValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro-----40
Db      163 CCCACCACTGCCGACGCTACAGTGAATGCAATGCCATTCATGTCAGAGGAGAGAG 222
Qy      41 -----CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57
Db      223 GTTCTCTCTCTTGCACAAATCTGCCCCAGCA-----CTTTT 261
Qy      58 GlyTyr---TrpPheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsn 76
Db      262 GGTACAGCTGTGTACAAAGG-----GAAAGAGTGGATGGC-----297

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REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-856B-2

Alignment Scores:
Score: 2.28e-08 Length: 1630
Percent Similarity: 187.00 Matches: 125
Best Local Similarity: 36.25% Conservative: 86
Query Match: 21.48% Mismatches: 206
Indels: 165
Gaps: 28

US-09-937-636-3 (1-512) x US-08-468-856B-2 (1-1630)

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QY      5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrIleArg 24
      |||||  ::|||
Db      127 CTGCTCACAGCCTCATCTTA-----ACCTTCTGGAAACCCG 162

QY      25 ValGlnGluSerValMetValProGluGlyLeuGlyIleSerValPro-----40
      ::|||  ::|||
Db      163 CCCACCACTGCCAGCTACTACTGAAATCCATTCATTCATTCGACAGAGGAGGAG 222

QY      41 -----CysSerPheSerTyrProArgGlnAspTyrThrGlySerThrProAlaTyr 57
      ::|||  ::|||
Db      223 GTTCTTCCTTCCTGTCACAAATCTGCCACAGCA-----CTTTT 261

QY      58 GlyIyr---TrrPheIysAlaValThrGluThrThrIlysglyAlaProValAlaThrAsn 76
      |||||  |||||
Db      262 GGCTACAGCTGTGTACAAAGG-----GAAAGAGTGATGTC-----297

QY      77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
      ::|||  ::|||
Db      298 -----AACCTCAATTTGTAGATATGCCAATAGGAATCAACAAGCTACCCGAGGCC 351

QY      97 AlaIysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
      |||||  |||||
Db      352 GCAAAACAGCGGTGCAGAGACAATATACCCCAATGCATCCGTGATCCAGAACGTCACC 411

QY      110 MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129
      |||||  ::|||
Db      412 CAGATGACACAGGATTTCTACACCTTACCAAGTC-----ATAAGTCAGAT 456

QY      130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149
      ::|||  ::|||
Db      457 CTGTGTGATGAA-----GAAGCACTGGACAGTTCCATGTATAC 495

QY      150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrrPala 169
      ::|||  ::|||
Db      495 -----495

QY      170 PheGluGluCysProProProSerPheSerTrrPheGlyAlaAlaLeuSerSerGlnGly 189
      |||||  |||||
Db      496 ---CCGGAGCTGCCAAGCCTCC-----ATCTCCAGCAACAC 531

QY      190 ThrIlyProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209
      ::|||  ::|||
Db      532 TTCAAACCTGTGGAGGACAAAGATGCTGTG---GCCTTCACTGTGAACGACGACGCTAG 588

QY      210 AspThrAspLeuThrCysHisValAspPheSerArgIlysglyValSerAlaGlnArgThr 229
      |||||  ::|||
Db      589 GACACAACTCACTGCTGGTGAATAACATCAGAGCCTCCGCGTACAGTCCC-----639

QY      230 ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
      |||||  ::|||
Db      640 ---AGGCTGACAGCTGTCCATGTGCAACAGACCTCACTACTGATGTCACAAAGGAT 696
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QY      249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr---267
      ::|||  ::|||
Db      697 GACACAGAGCCCTTGTAGTGTGAATATACAGAACCACTGAT---GGCAACCGAGTGAC 753

QY      268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu-----282
      |||||  |||||
Db      754 CCAGTCACCTGATGATGCACTATGAGCCCGGACACCCACCATTTCCCTTCAGACACC 813

QY      283 -----GlyGlnSerLeuCysLeuValLysValThrHisSerSerProPala 298
      |||||  |||||
Db      814 TATTACCTCCAGGAGGAGAACTCAGCTCTCTGCTATGACGCTTAAACCACTGCA 873

QY      299 ArgLeuSerTrrPheGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
      ::|||  ::|||
Db      874 CAGTACTCTCTGCTTATCATGTGAACATTCACAGAACGACACAGAG-----921

QY      319 ValLeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArg 338
      |||||  ::|||
Db      922 ---CTCTTATCCCTAATCATCTGTGAATATAGTGAATCCATACCTGACGACCAAT 978

QY      339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTyrLysGly 357
      ::|||  ::|||
Db      979 AACCTCACTGCTGCTCAACAGACCACTGCT-----AAGACG 1017

QY      358 LeuIleSerThrAlaPheSer-----364
      |||||  |||||
Db      1018 ATCATAGTCACTGAGCTAAGTCCAGTAGTACCAAGCCCAATCAAAAGCCAGCAAGACC 1077

QY      365 -----AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAla 382
      |||||  ::|||
Db      1078 ACAGTCAAGAGAGATTAAGAGACTGTGTGAACCTGACC-----TGCTCCACA 1122

QY      383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrPro 399
      |||||  |||||
Db      1123 AATGACACTGGAATCTCATTCGTTGGTCTTCAAAAACGAGATCCCTGCTCGAG 1182

QY      400 ArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValPro-ThrAl 419
      |||||  ::|||
Db      1183 AGATGAAGAGCTGCTCCAGGACACACACCTC-----ACATTAACCTGTGCAAG 1233

QY      419 aglyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLe 439
      ::|||  ::|||
Db      1234 AGGAGAGATGCTGGACGATGTTGTGTGAGGCTTTCACCAATCACTAGAACCAAGC 1293

QY      439 uProProGlyAlaProSerProGluSerLysAsnGlnLysLysGlnTyrGln-----457
      |||||  |||||
Db      1294 GACCCCATCATGCTGAACGTAACTATTAATCTTACACAGAAATAATGGCTCTCACT 1353

QY      458 -----LeuProSerPhePro-----462
      |||||  |||||
Db      1354 GGGGCCATTTGCTGGCATTTGTGATGTAGTGGCCCTGGTGTGTGATAGCAGTAGCC 1413

QY      463 -----GluProLysSerSerThrGlnAlaProGluSerGln 474
      |||||  |||||
Db      1414 CTGGCATGTTTCTGCAATTTTGGGAAGACCGGACGCTCAGACCACTCCAAATGACCCACC 1473

QY      474 ngluSerGlnGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgPro---Ar 493
      ::|||  ::|||
Db      1474 TAAACAAGTGAATGAATGATTAATTTACCTGATTAAGCCCAAGCCAGCAACACAGCA 1533

QY      493 gProGluAlaArgMetProLys-----GlyThrGlnAlaAspTyrAlaGluValLysPh 511
      |||||  ::|||
Db      1534 ACCAATCTCAAGCTCCCATCCATCCCTAACAGCCAGAAATATTAATTCAGAAATGAAAAA 1593

QY      511 eGln 512
      |||||
Db      1594 GCAG 1597
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RESULT 9
US-08-468-856A-2
Sequence No. 2, Application US/08468859A
Patent No. 6022958

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GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Eiting, James; Kamarek, Michael;
APPLICANT: Kreschmer, Axel
TITLE OF INVENTION: CDNA CODING FOR MEMBERS OF THE
NUMBER OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: Wordperfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468, 859A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027, 974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760, 031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274, 107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207, 678
FILING DATE: 16-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/060, 031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016, 683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896, 361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-859A-2

Alignment Scores:
Pred. No.: 2,28e-08 Length: 1630
Score: 187.00 Matches: 125
Percent Similarity: 36.25% Conservative: 86
Best Local Similarity: 21.48% Mismatches: 206
Query Match: 6.91% Indels: 165
DB: 3 Gaps: 28

US-09-937-636-3 (1-512) x US-08-468-859A-2 (1-1630)

QY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyAlaArgPheTrpIleArg 24
DB 127 CTGCTCACAGCCTCACTCTTA-----ACCTTCGGAACCCG 162
QY 25 ValGlnGluSerValMetValProGlnGluGlyLeuGlySileSerValPro----- 40

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DB 163 CCCACACAGCCCGACGTACTAGTAATGCATGCCATTCGAATGTCGACAGGGGAGAGAG 222
QY 41 -----CysSerPheSerTrpProArgGlnAspTrpThrGlySerThrProAlaTrp 57
DB 223 GTTCTTCCTTCCTTGTCACCAATCTGCCCGACGAA-----CTTTT 261
QY 58 GLTYR-----TriPheLysAlaValThrGluTrpThrLysGlyAlaProValAlaThrAsn 76
DB 262 GGTACAGCTGGTGTACAAAGG-----GAAGAAGTGGATGCG----- 297
QY 77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
DB 298 -----AACGTCGAATGTAGATATGCAATAGCAATCAACAAGCTACCCAGGCCGCC 351
QY 97 AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
DB 352 GCAACACGGCGTCGAGAGACAATATACCCCAATGCATCCCTGCTGTCGACGAAAGTCAC 411
QY 110 MetGlnAspGluSerGlnTrpPhePheArgValGluArgGlySerTrpValAlaArgTrpAsn 129
DB 412 CAGATGACACAGAGATTCTACACCTACAAATC-----ATAAGTCAGAT 456
QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTrp 149
DB 457 CTTGTGAATGAA-----GAAGCAACTGAGCAAGTTCATGTATAC 495
QY 150 IleProGluThrLeuGluProGlyIleProValThrValIleCysValPheAsnTrpAla 169
DB 495 ----- 495
QY 170 PheGluGluCysProProSerPheSerTrpThrGlyAlaAlaLeuSerGlnGly 189
DB 496 ---CCGAGCTGCGCCAGCCCTCC-----ATCTCCAGCAACAC 531
QY 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAsnHis 209
DB 532 TCCAAACCCGTGGAGACAAAGATGCTGTG---GCCCTTCACTGTCGAACCTGAGACTGAC 588
QY 210 AspThrAspLeuThrCysHisValAspPheSerArgGlyValSerAlaGlnArgThr 229
DB 589 GACACAACTTACCTGTGTGATTAACAATCAAGACCTCCCGCTGCC----- 639
QY 230 ValArgLeuArgValAlaLeuTrpAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
DB 640 ---AGCTGACACTGTCATGCAATGCAACAGACCTCACTCTACTGCTACAAAGGAAT 696
QY 249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267
DB 697 GACACAGAGACCTATGAGTGTGAATATACGAACCCAGTGTAGT---CCGAACCGCACTGAC 753
QY 268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu----- 282
DB 754 CCAGTCACCTTGAATGTCAACTATGCGCCGACACCCCAACCATTTCCCTTCACAGACCC 813
QY 283 -----GlyGlnSerLeuCysLeuValGlyValThrHisSerSerProProAla 298
DB 814 TATTAACGTCACAGGGGAAACCTCAGCCTCTCTGCTATAGCAAGCCCTAACCCCTGCA 873
QY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerArgProGly 318
DB 874 CAGTACTCTGCTGTATCAATGCAATTCACCAACCAAGACACACAGAG----- 921
QY 319 ValLeuGluLeuProArgValGlnValGluHisGlyGlyGluPheThrCysHisAlaArg 338
DB 922 ---CTCTTATCCCTTCAATCACTGTGATATAGTATAGTCCATATCTGCACAGCCCAAT 978
QY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpTrpLysGly 357
DB 979 AACTCAGTCACTGGCTGCAACAGAGACCAAGTCACT-----AAGAGC 1017
QY 358 LeuIleSerThrAlaPheSer----- 364

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Db 1018 ATCATAGTCACTGAGCTAAGTCCAGTAGTACCAAGCCCAATCAAGACGACGAGACC 1077
QY 365 -----AsnGlyAlaPheLeuGlyIleThrAlaLeuLeuPheLeuGlyLeuAla 382
Db 1078 AAGAGTCACAGAGATGAGAGACTCTGTGAACCTGACC-----TGTCTCCACA 1122
QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrGlnThrPro 399
Db 1123 AATGACACTGGAATCTCCATCGTGGTTCCTCAAAACAGAGCTCCCGCTCGGAG 1182
QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValAlaPro--ThrAl 419
Db 1183 AGGATGAAAGCTGTCCAGGCAACACCCCTC-----AGCATAAACCCCTGTCAAG 1233
QY 419 aGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLe 439
Db 1234 AGCGAGAGATGCTGGGACGATATGTGTAGGCTTCAACCCCAATCAGTAGAACCAAGC 1293
QY 439 uProGlnAlaProSerProGlnSerLysAsnGlnLysGlnTyrGln----- 457
Db 1294 GACCCATCAATGCTGAAGCTAAATATATGCTACCAAGAAATGGCCTCACACT 1353
QY 458 -----LeuProSerPhePro----- 462
Db 1354 GGGCCATTGCTGCATTGTGATGAGTACGTGGCTGCTGTGATAGCAGTAGACC 1413
QY 463 -----GluProLysSerSerThrGlnAlaProGlnSerGln 474
Db 1414 CTGGCATGTTTTCGATTTGGGGAAGCGGACGCTGAGCAGCAGCAGTCCATGCCACC 1473
QY 474 nGlnSerGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlnValAlaArgPro--Ar 493
Db 1474 TAACAAGATGATAGTAACTTACTTATCTACCTGATGACCTTGAAGCCAGCAACCCACACA 1533
QY 493 gProGlnAlaArgMetProLys-----GlyThrGlnAlaAspTyrIleGlnValLysPhe 511
Db 1534 ACCAAGCTCAGCCCTCCCATCCCTACAGCCAGCAAGAAATATTATTTCAGATTAAGAAA 1593
QY 511 eGln 512
Db 1594 GCAG 1597

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RESULT 10
US-08-468-856B-1
: Sequence 1, Application US/08468856B
: Patent No. 6013772
: GENERAL INFORMATION:
: APPLICANT: Barnett, Thomas; Elting, James; Kamarch, Michael;
: APPLICANT: Kretschmer, Axel
: TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
: TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sprung Horn Kramer & Woods
: STREET: 660 White Plains Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591-5144
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
: OPERATING SYSTEM: SYSTEM 7.5
: SOFTWARE: WordPerfect 3.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,856B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/027,974
: FILING DATE: 08-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/760,031

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: FILING DATE: 13-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/274,107
: FILING DATE: 21-NOV-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/207,678
: FILING DATE: 16-JUN-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/060,031
: FILING DATE: 19-JUN-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/016,683
: FILING DATE: 19-FEB-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/896,361
: FILING DATE: 13-AUG-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurt G. Briscoe
: REGISTRATION NUMBER: 33,141
: REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 332-1700
: TELEFAX: (914) 332-1844
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3173 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-468-856B-1
: Alignment Scores:
: Pred. No.: 1.04e-07 Length: 3173
: Score: 185.00 Matches: 120
: Percent Similarity: 35.04% Conservative: 72
: Best Local Similarity: 21.90% Mismatches: 180
: Query Match: 6.84% Indels: 176
: DB: Caps: 28
: US-09-937-636-3 (1-512) x US-08-468-856B-1 (1-3173)
: QY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrPleArg 24
: Db 127 CTGCTCAGACCGCTCAGCTCTA-----ACCTCTGGAACCG 162
: QY 25 ValGlnGlnSerValMetValProGlnGlyLeuGlyIleSerValPro----- 40
: Db 163 CCCACACACTGCCCCAGCTCAGTCAATCCATTCATGTTGCAGAGGGGAAGAG 222
: QY 41 -----CysSerPheSerTyrProArgGlnAspTyrThrGlySerThrProAlaTyr 57
: Db 223 GTTCTTCTCCTGCTCCACAAATGCCCCAGCA-----CTTTT 261
: QY 58 GlyTyr---TyrPheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsn 76
: Db 262 GGCTACAGCTGTGTAACAAAGG-----GAAGAGTGATGGC----- 297
: QY 77 HisGlnSerArgGlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
: Db 298 -----AACCGTCAATTTAGATATGCAATAGGAGACTCAACAAAGCTCCAGGCCCC 351
: QY 97 AlaLysGly-----AsnGlySerLeuValIleArgAspAlaGln 109
: Db 352 GCAAACAGCGGTGAGAGACAATATATCCCAATGATCCCTGCTGATCCAGAACGTACAC 411
: QY 110 MetGlnAspGlnSerGlnTyrPhePheArgValGlnArgGlySerTyrValArgTyrAsn 129
: Db 412 CAGATGACACAGAAATTTCAACCTTACAGTC-----ATAAGTCAGAT 456
: QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149
: Db 457 CTGTGTAATGAA-----GAAGCACTGAGACAGTTCCATGTATAC 495

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OY 150 lIeProgluThrLeuGlueProgluGlnProvalThrValIleCysValPheAsnTrpAla 169
DB 495 -----
OY 170 PheGlueGluCysProProserPheSerTrpThGlyAlaAlaLeuSerGlnGly 189
DB 496 ---CCGGAGCTGGCCCAAGCCCTCC-----ATCTCCACCAACAC 531
OY 190 ThrLysProThrThrSerHisPheSerIleLeuSerPheThrProArgProGlnAspHis 209
DB 532 TCACACCTCTGTGGAGACAAGCATGCTGTGGCTCC---ACCTGTACACCTGTAGACTCAG 588
OY 210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229
DB 589 GACACACCTACTGTGGTGGATTAACATCAAGAGCTCCCGGTGACTGCC----- 639
OY 230 ValArgLeuArgValAlaTrpAlaProAlaGaspLeu---ValIleSerIleSerArgAsp 248
DB 640 ---AGGCTCAGCTGTCCATGCGCAACAGACCCCTACTCTACTCAGTGTACACAGAAAT 696
OY 249 AsnThr---ProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267
DB 697 GACACAGACCCCTATAGTGTGAAATACAGAACCCAGTGTGAGTCCGAACCTCAGTACACCA 756
OY 268 ValLeuGluAsnLeuGlnGlyThrSerLeuProValLeuGlu----- 282
DB 757 GTACACTTGATTCACACTATGCGCGGACACCCCACTTCCCTCCAGACACTAT 816
OY 283 -----GlyGlnSerLeuCysLeuValCysValThrHisSerSerProAlaArg 299
DB 817 TACCGTCAGGCGCAACCTCAGCCTCTGCTGATGACAGCCTTAACCCAGCTGCAG 876
OY 300 LeuSerTrpThrGlnArgGlnValLeuSerProSerGlnProserAspProGlyVal 319
DB 877 TACTCTGGCTTATCAATGGACATTCACAGCAACCAAG----- 921
OY 320 LeuGluLeuProArgValGlnValGlnHisGlnGlyGluPheThrCysHisAlaArgHis 339
DB 922 CTCTTTATCCCTAACATCACTGTGAAATAGTGAAATCCATACCTGCGCAGCCCAAT 981
OY 340 ProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpLysGlyLeu 358
DB 982 TCAGTCAGCGCTGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1041
OY 359 ---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyIleThrAla 375
DB 1042 CCACAAGAAATGGCTCTCACCCTGGGCGCATTTCTGCGATTTGGAGTAGTGCC 1101
OY 376 LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeu----- 389
DB 1102 CTGGTTGCTCTG---ATAGCAGTAGCCCTGCGCATGTTTCTGCATTTCCGGAGACCGGC 1158
OY 390 -----ProLysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSer 407
DB 1159 AGGCAAGCAGCAGCGGTGATCTCACAGAG---CACAAACCCCTCAGCTCCACACACACT 1215
OY 408 ThrIleLeuAspTrpIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn 427
DB 1216 CAG-----GACCACATCCAAAT----- 1230
OY 428 GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
DB 1231 -----GACCCACCT 1239
OY 448 SerLysLysAsnGlnLysLysGlnTrpGlnLeuProSerPheProGluProLysSerSer 467
DB 1240 AACAAAGATGAAT----- 1251
OY 468 ThrGlnAlaProGluSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 487
DB 1252 -----GAGGTTCCTTATTTCTACCTGACTTT 1278
OY 488 ProGlyValArgPro---ArgProGluAlaArgMetProLys-----GlyThrGlnAla 504

```

```

DB 1279 GAAGCCAGCAACCCACACACCACTTCAAGCTCCCATCCCTAACAGCCACAGAAATA 1338
OY 505 AspTrpAlaGluValLysPheGln 512
DB 1339 ATTATTCAGAGTAAAAAAGCAG 1362

RESULT 11
US-08-468-859A-1
; Sequence 1, Application US/08468859A
; Patent No. 6022958
; GENERAL INFORMATION:
; APPLICANT: Barnet, Thomas; Eiling, James; Karmark, Michael;
; APPLICANT: Kriesscher, Axel
; TITLE OF INVENTION: CDNA CODING FOR MEMBERS OF THE
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Horn Kramer & Woods
; STREET: 660 White Plains Road
; City: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,859A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760,031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274,107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207,678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060,031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016,683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896,361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3173 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-468-859A-1

Alignment Scores:
Pred. No.: 1.04e-07 Length: 3173
Score: 185.00 Matches: 120
Percent Similarity: 35.04% Conservative: 72

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Best Local Similarity: 21.90% Mismatches: 180
 Query Match: 6.84% Indels: 176
 DB: 3 Gaps: 28

US-09-937-636-3 (1-512) x US-08-468-859A-1 (1-3173)

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OY      5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrPileArg 24
      127 CTGCTCAGACGCTCCTCTCTA-----ACCTTCTGGAACCG 162
      25 ValGlnGlnSerValMetValProGlnGlyLeuGlyIleSerValPro-----40
      163 CCCACCACTGCCACCACTACTACTACTATCCATCCATCCATCCATCCAGAGGAGAGAG 222
      41 -----CysSerPheSerTyProArgGlnAspTrpGlnGlySerThrProAlaTy 57
      223 GTTCTTCTCTCTGTCACAAATCTGCCACAGCA-----CTTTT 261
      58 GlyTyT---TrpPheLysAlaValThrGlnThrLysGlyAlaProValAlaThrAsn 76
      262 GGTACACAGCTGTACAAAGG-----GAAAGAGTGATGCC-----297
      77 HisGlnSerArgGlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
      298 -----AACGTCAAATTTGTAGATAGCAATAGCACTACCAAGCTACCCAGGCGCC 351
      97 AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
      352 GCAAAACAGCGGTGAGACACAATATACCCCAATGATGATCCGTGCTGATCCAGAGCTCAC 411
      110 MetGlnAspGlnSerGlnTyPhePheArgValGlnArgGlySerTyValArgTyAsn 129
      412 CAGAAATGACACAGAAATTTCTACACCTTACAGTC-----ATAAGCAGAT 456
      130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTy 149
      457 CTGTGATGAA-----GAGCACTGGACACTTTCATGTATAC 495
      150 IleProGlnThrLeuGlnProGlyGlnProValThrValIleCysValPheAsnTrpAla 169
      495 -----495
      170 PheGlnGlnCysProProProSerPheSerTrpThrGlyAlaIleLeuSerSerGlnGly 189
      496 ---CCGAGCTGCCCAAGCCCTCC-----ATCTCAGCAACAAAC 531
      190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209
      532 TCCAAACCTGTGAGAGCAAGATGCTGTGCCCTCC---ACCTGTGAACCTGAGACTCAG 588
      210 AspThrAspLeuThrCysHisValAspPheSerArgGlyGlyValSerAlaGlnArgThr 229
      589 GACCAACACTACTCTGTGGTGAATAACAATCAGAGCCCTCCGGTCAGTCCC-----639
      230 ValArgLeuArgValAlaTyAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
      640 ---AGGTGAGCTGCTCAATGCAACAGAGCCCTCACTACTACTACTAGTGCACAGAGAT 696
      249 AsnThr---ProAspProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThr 267
      697 GACACAGAGACCTTGTAGTGAATACAGAACCACTGAGTGGAAACCTCAGAGACCA 756
      268 ValLeuGlnAsnLeuGlnGlyAsnGlyThrSerLeuProValLeuGln-----282
      757 GTCACTTGAATGTACACTATGGCCGAGACACCCCAACATTTCCCTTCGAGACACTAT 816
      283 -----GlyGlnSerLeuCysLeuValCysValThrHisSerSerProAlaArg 299
      817 TACCGTCCAGGGGCAACCTCAGCTCTCTCTGCTATCAGAGCTTACACCACTGACAG 876
      300 LeuSerTrpThrGlnArgGlnValLeuSerProSerGlnProSerAspProGlyVal 319
      877 TACTCTGGCTTATCAATGGAACATTCACAGCAAGACACACAAAG-----921
  
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OY      320 LeuGlnLeuProArgValGlnValGlnHisGlnGlyGlnPheThrCysHisAlaArgHis 339
      922 CTCTTATCCCTAACATCATCTGTGAATATAGTGAATCTTACTTGGCAGCCCAATATAC 981
      340 ProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTyLysLysGlyLeu 358
      982 TCAGTCACTGGTGCACAGAGCACACAGTCAAGACATGATGATGATGATGATGATGAT 1041
      359 ---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyIleThrAla 375
      1042 CCACAAGAAAATGGCTCTCAGCTGAGCCATGCTGCTGATGATGATGATGATGATGATG 1101
      376 LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeu-----389
      1102 CTGTGTGCTG---ATAGCAATGACCTGTCGATGCTTCTGCTGATGCTGCGAAGACCGC 1158
      390 -----ProLysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSer 407
      1159 AGGCAAGCAGACACGCGTGAATCTCAGAG---CACAAACCTCAGTCTCCACCACT 1215
      408 ThrIleLeuAspTyIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn 427
      1216 CAG-----GACCACTCCAAAT-----1230
      428 GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
      1231 -----GACCACCT 1239
      448 SerLysLysAsnGlnLysGlnTyGlnLeuProSerPheProGluProLysSerSer 467
      1240 AACAAAGATGAT-----1251
      468 ThrGlnAlaProGlnSerGlnGlnSerGlnGlnLeuHisTyAlaThrLeuAsnPhe 487
      1252 -----GAGTACTTATTTCACTTCACTTCACTT 1278
      488 ProGlyValArgPro---ArgProGlnAlaArgMetProLys-----GlyThrGlnAla 504
      1279 GAAGCCAGCAACCCACACCAACCACTTACCTGCTCCATCCATCCATCCATCCATCC 1338
      505 AspTyAlaGlnValLysPheGln 512
      1339 ATTATTTCAGAAATGTAAGAAAGCAG 1362
  
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RESULT 12
 US-08-468-856B-6
 ; Sequence 6, Application US/08468856B
 ; Patent No. 6013772
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;
 ; APPLICANT: Kretschmer, Axel
 ; TITLE OF INVENTION: CDNA CODING FOR MEMBERS OF THE
 ; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Spring Horn Kramer & Woods
 ; STREET: 660 White Plains Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10591-5144
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 ; OPERATING SYSTEM: SYSTEM 7.5
 ; SOFTWARE: WordPerfect 7.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,856B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/027,974

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: FILING DATE: 08-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/760,031
: FILING DATE: 13-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/274,107
: FILING DATE: 21-NOV-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/207,678
: FILING DATE: 16-JUN-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/060,031
: FILING DATE: 19-JUN-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/016,683
: FILING DATE: 19-FEB-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/896,361
: FILING DATE: 13-AUG-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: KURT G. BRISCOE
: REGISTRATION NUMBER: 33,141
: REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 332-1700
: TELEFAX: (914) 332-1844
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3461 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-468-856B-6

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Alignment Scores:
Pred. No.: 1.2e-07 Length: 3461
Score: 185.00 Matches: 130
Percent Similarity: 34.65% Conservative: 80
Best Local Similarity: 21.45% Mismatches: 200
Query Match: 6.84% Indels: 196
DB: 3 Gaps: 31

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US-09-937-636-3 (1-512) x US-08-468-856B-6 (1-3461)

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QY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheTrpIleArg 24
   ||||| :||| |||||
DB 127 CTGCTCACAGCCTCTCTCTA-----ACCTTCTGGAAACCG 162

QY 25 ValGlnGluSerValMetValProGlnGlyLeuCysIleSerValPro----- 40
   :|: :|: ||| :|: :|:
DB 163 CCCACACAGCCGACGCTACTGATGCAATGCCATTCATCTTCCAGAGGGAAGAG 222

QY 41 -----CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57
   :|: :|: ||| :|: :|:
DB 223 GTTCTTCTCTGTCTGCACAACTGCCCCAGCAA-----CTTTT 261

QY 58 GlyTyr---TrpPheLysAlaValThrGlnTrpThrLysGlyAlaProValAlaTrpAsn 76
   ||||| :||| :|: ||| :|:
DB 262 GCTCTACAGCTGGTACAAAGG-----GAAAGAGTGGATGG----- 297

QY 77 HisGlnSerArgGluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
   :|: :|: ||| :|: :|:
DB 298 -----AACCGTCAATTTAGATATGCAATAGCAATCAACAAACGCTACCCAGGCCC 351

QY 97 AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
   ||| :|: ||| :|: ||| :|:
DB 352 GCAACACAGCGGTGAGAGACAATATACCCCAATGCATCCCTGTGATCCAGAACTGACAC 411

QY 110 MetGlnAspGluSerGlnTyrPhePheArgValGlnArgGlySerTyrValArgTyrAsn 129
   ||| :|: ||| :|: ||| :|:
DB 412 CAGATGACACAGGATTTACACCTTACACAGTC-----ATAAGTCAAGAT 456

QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149

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```

DB 457 CTTGTGAATGAA-----GAAGCAACTGACGACGTTTCATGTATAC 495
   :|: :|: ||| :|: :|:
QY 150 IleProGlnThrLeuGluProGlnIleProValThrValIleCysValPheAsnTrpAla 169
   :|: :|: ||| :|: :|:
DB 495 ----- 495

QY 170 PheGlnGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189
   ||| ||| |||||
DB 496 ---CCGACCTGCCCCAAGCCCTCC-----ATCTCCAGCAACAC 531

QY 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAsnHis 209
   :|: :|: ||| :|: :|:
DB 532 TCCACCCCTGTGGAGACAAAGATGCTGG---GCTTACCTGTAACCTGAGACTGAC 588

QY 210 AspThrAspLeuThrCysHisValAspPheSerArgGlyValSerAlaGlnArgThr 229
   ||||| :|: :|: ||| :|:
DB 589 GACACAACCTTACTGTGTGATAAACAATACAGAGCCCTCCGCTCAGTCCC----- 639

QY 230 ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
   ||||| :|: :|: ||| :|:
DB 640 ---AGGCTCAGCTGTCCAAATGGCAACAGAGACCCCTACTCTACTGTCACACAGAAAT 696

QY 249 AsnThrProAspProProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThr--- 267
   :|: :|: ||| :|: :|:
DB 697 GACACAGACACCCATGATGATGTAATACAGAACCCAGTGA---GCCAAACCCAGCTGAC 753

QY 268 ---ValLeuGlnAsnLeuGlnGlyThrSerLeuProValLeuGlu----- 282
   ||| :|: :|: ||| :|:
DB 754 CCAGTCACCTGTGATGCTCATGTCGCGGACACCCACCACTTCCCTTCAGACACC 813

QY 283 -----GlyIleSerLeuCysLeuValCysValThrHisSerSerProProAla 298
   ||| :|: :|: ||| :|:
DB 814 TATTACCGTCCAGGGGCAACCTCAGCTCTCTCTGTATGACAGCTTAAACCCCTGCA 873

QY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
   :|: :|: ||| :|: :|:
DB 874 CAGTACTCTGTGGTTTCAATGACATTCACAGCAACAGCACAAAG----- 921

QY 319 ValLeuGlnLeuProArgValGlnValGlnHisGlnGlyLeuPheThrCysHisAlaArg 338
   ||| :|: :|: ||| :|:
DB 922 ---CTCTTATCTCCCTCAATCATGATGAAATAGTGAATGCTTACCTGCGCCAGCCAAAT 978

QY 339 HisProLeu---GlySerGlnHisValSerLeuSerValHisTyrLysGly 357
   :|: :|: ||| :|: :|:
DB 979 AACTGACGCTGCTGCAACAGACCAACAGTC-----AAGACG 1017

QY 358 LeuIleSerThrAlaPheSer----- 364
   :|: :|: ||| :|: :|:
DB 1018 ATCATATGTCACGAGCTAAGTCCAGTAGACAAACCCCAATCAAAAGCAGACAGAC 1077

QY 365 -----AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAla 382
   ||| :|: :|: ||| :|:
DB 1078 ACAGTCCACAGAGATAGAGACTCTGGAACCTGACC-----TGCCTCCACA 1122

QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrGluTrpPro 399
   ||| :|: :|: ||| :|:
DB 1123 AATGACACTGGAATTCCTCATCTGCTTCTTAAAAACCAAGAGTCTCCCGTCTGGAG 1182

QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValAlaPro----- 417
   :|: :|: ||| :|: :|:
DB 1183 AGGATGAGACTGCTCCAGGCAACACCAACCCCTGACG---ATAAACCTGTCAAGAGGAG 1239

QY 418 -----ThrAlaGlyPro 421
   :|: :|: ||| :|: :|:
DB 1240 GATGCTGGAGCGTATTGCTGTGAGGCTTTCACCAACCAATAGTAAGAACAACCAAGCCGCC 1299

QY 422 LeuAlaGlnLysArgAsnGlnLysAlaTrpProAsnSerProArgThrProLeuProPro 441
   :|: :|: ||| :|: :|:
DB 1300 ATCATGCTGAACGTAAACTATATATGCTTACCACAA-----GAAATAGGCTCTGACCT 1353

QY 442 GlyAla----- 443
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QY 249 AenThrProAspProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr--- 267
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   697 GACACGAGACCTATGAGTGTGAATATACAGAAACCCAGTAGT---GCGAACCAGCAGTGCAC 753
QY 268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu----- 282
   |||||
   754 CCAGTCACCTGTAATGTACACTATGGCCCGGACACCCACCATTTCCCTTCAGACACC 813
QY 283 -----GlyGlnSerLeuGlyValGlyValThrHisSerSerProProAla 298
   |||||
   814 TATTACCGTCCAGGGGCAACCTCAGCCTCTCTCTATGACGCCCTGATCCACCTGCA 873
QY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
   |||||
   874 CAGTACTCTGCTGCTATCATAGAACATTCACCAAGACACACAGAG----- 921
QY 319 ValLeuGluLeuProArgValGlnValGlnHisGlyGlyGlnPheThrCysHisAlaArg 338
   |||||
   922 ---CTCTTATCCCTTAACATCATCTGATTAATAGTGATCTGATACCTGACCGCCAAAT 978
QY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpLysGly 357
   |||||
   979 AACTAGTCTACTGCTGCAACAGACAGACAGATC-----AAGAGC 1017
QY 358 LeuIleSerThrAlaPheSer----- 364
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   1018 ATCATAGTCTACTGAGCTAGTCACTAGTACCAAGACCCCAATCAACACGACAGAGACC 1077
QY 365 -----AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuGlyLeuAla 382
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   1078 ACAGTCACAGAGATAGAGACTGTGTGAACCTGACC-----TGCTCCACA 1122
QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrGlnThrPro 399
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   1123 AATGACACTGGAAATTCCTCCATCGGTGGTCTTCAAAACCAACCTCCCGTCCCTGGAG 1182
QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTrpIleAsnValAlaPro----- 417
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   1183 AGGATGAAGCTGTCCAGGGCAACACACCTCAGC---ATTAACCCCTGCAAGAGGGAG 1239
QY 418 ----- 421
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   1240 GATGCTGGAGCTATTGGTGTAGGTCTTCAACCCAAATCAGTAGAAGCAAGCGACGCC 1299
QY 422 LeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuProPro 441
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   1300 ATCATGCTGACAGCTAACTATATAGCTCTACCAAA-----GAAATGGCCTCTCAGCT 1353
QY 442 GlyAla----- 443
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   1354 GGGGCCATTGCTGGCATTGTGATGTAGTAGTGGCCCTGTGCTGTATAGCAATGAGCC 1413
QY 444 -----ProSerProGluSerLysAsn 451
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   1414 CTGGCATGTTTTCTCATTTCCGGAAGACCGGAGGCGACGACGCGATGATCTCACA 1473
QY 452 GlnLysGlnLysGlnLeuProSerPheProGluProLysSerSerThrGln----- 469
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QY 470 AlaProGluSerGlnLysGlnLysGlnLysLysAlaThrLeuAsnPheProGly 489
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QY 490 ValAlaGPro---ArgProGluAlaArgMetProLys-----GlyThrGlnAlaAspTrp 506
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QY 507 AlaGluValLysPheGln 512
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   1633 TCAGAAAGTAAAAAAGCAG 1650

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RESULT 14

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US-08-408-095-30
; Sequence 30, Application US/08408095
; Patent No. 585678
; GENERAL INFORMATION:
; APPLICANT: Chinadural, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,095
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1503
; US-08-408-095-30
; US-08-408-095-30 (1-512) x US-08-408-095-30 (1-2166)
Alignment Scores:
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Score: 177.50 Matches: 116
Percent Similarity: 35.49% Conservative: 76
Best Local Similarity: 21.44% Mismatches: 175
Query Match: 6.56% Indels: 175
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QY 44 -----SerTrpProArgGlnAspTrpThrGlySerThrProAlaTrpGlyTrp 59
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   298 TCACGTAAACCCAGTGTTCACCGGTATGATG-----AAACCCCAATGGCGCC 345
QY 60 TrpPheLysAlaVal-----ThrGluThrThrLysGlyAlaProValAlaThrAsn 76
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   346 TGGGA-GAGGACCATCGCTTGGGGGTGCTGAAGATCCAAACCTTGGCGGACACACAC 404
QY 77 HisGlnSerArgGluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
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   405 CATCGCTCTCGC-----ACGTGTAAATAGTTGAGTCTCTCGGCGCTCGCC 449
QY 97 AlaLysGlyAsnCysSerLeu-ValIleArgAspAlaGlnMetGlnAspGluSerGlnTrp 116
   |||||
   450 TGTGCGCTGAATGTCTCACTATGCCCCCGAGACGCTGAGGCTCGG----- 495
QY 116 rPhePheArgValGluArgGlySerTrpValArgTrpAsnPheMetAsnAspGlyPhePh 136

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OY	222	lysglyalseralaglntgthvalargleuargvalalatyratalproalargleu	241
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Db	684	-----ccagtcagggagccctggcctcagagggcattcagctttggt	728
OY	262	serglinalaasnargthvalleuagluasnleuglyasnlythrserleuprovalleu	281
Db	729	gagcctgaaagctggaata-----gtcgct	752
OY	282	gluglylnserleucysyleuvalcysvalthnhtsererproalalargleuser	301
Db	753	ccctggaggaatgactgacttcaccttcacattcctccagagccctccctcagaggtccac	812
OY	302	trpthrglnarguglinalleuserproserlproserasrproglualleuglu	321
Db	813	tggatlaaagatggtgcaccccttg-----gctcctctc	863
OY	322	leuproargvalcinalagluynlaglucyluetherhrcysnlsaladrgnleu	341
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OY	388	lleuaprolysarargthrglnthrglnthrproalargrpheserarghtsler	407
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OY	448	serlylsyaasnclnlyslglnlycglndeuproserpherpogluprolysesser	467
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Search completed: October 8, 2003, 22:42:57
Job time : 139 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:05:43 : Search time 414 Seconds
(without alignments)
3209.042 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO.spool/US09937636/runat_08102003_083237_24/app.query.fasta_1.711
-DB-Published_Applications_NA -QFMT-fastlap -SUFFIX-p2n.rnpb -MIMMACH-0.1
-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR SCORE-pct -THR MAX-100
-THR MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-p2n -NORM-ext -HEARSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09937636 -RCN_1_1_271 -runat_08102003_083237_24
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FEAPOP-6 -FEAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2580.5	95.4	2208	11	US-09-910-600-15 Sequence 15, Appl

2	2580.5	95.4	3024	11	US-09-910-600-27 Sequence 27, Appl
3	2576.5	95.2	2338	11	US-09-984-130-148 Sequence 148, App
4	2278	84.2	2265	10	US-09-910-600-1 Sequence 1, Appl
5	2265	83.7	2764	10	US-09-978-295A-258 Sequence 258, App
6	2265	83.7	2764	10	US-09-978-697-258 Sequence 258, App
7	2265	83.7	2764	10	US-09-978-192A-258 Sequence 258, App
8	2265	83.7	2764	10	US-09-999-832A-258 Sequence 258, App
9	2265	83.7	2764	11	US-09-978-189-258 Sequence 258, App
10	2265	83.7	2764	11	US-09-978-608A-258 Sequence 258, App
11	2265	83.7	2764	11	US-09-978-585A-258 Sequence 258, App
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31	2265	83.7	2764	12	US-10-143-030A-258 Sequence 258, App
32	2265	83.7	2764	12	US-10-199-672-117 Sequence 117, App
33	2265	83.7	2764	12	US-10-187-749-117 Sequence 117, App
34	2265	83.7	2764	12	US-10-194-457-117 Sequence 117, App
35	2265	83.7	2764	12	US-10-145-128A-258 Sequence 117, App
36	2265	83.7	2764	12	US-10-184-642-117 Sequence 117, App
37	2265	83.7	2764	12	US-10-196-747-117 Sequence 117, App
38	2265	83.7	2764	12	US-10-173-689-117 Sequence 117, App
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40	2265	83.7	2764	12	US-10-173-691-117 Sequence 117, App
41	2265	83.7	2764	12	US-10-173-692-117 Sequence 117, App
42	2265	83.7	2764	12	US-10-173-694-117 Sequence 117, App
43	2265	83.7	2764	12	US-10-173-698-117 Sequence 117, App
44	2265	83.7	2764	12	US-10-173-699-117 Sequence 117, App
45	2265	83.7	2764	12	US-10-173-707-117 Sequence 117, App

ALIGNMENTS

RESULT 1
US-09-910-600-15
Sequence 15, Application US/09910600
Publication No. US2003036631A1
GENERAL INFORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
TITLE OF INVENTION: NOVEL SINGLETS AND USES THEREOF
FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 2208
TYPE: DNA
ORGANISM: Homo sapiens
US-09-910-600-15

Alignment Scores: 5.01e-253 Length: 2208
Pred. No.: 2580.50 Matches: 510

Not Recd

QY 376 LeuLeuPheLeuCysLeuAlaLeuIlelleMetLysIleLeuProLysArgArgThrGln 395
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 QY 396 ThrGluThrProArgProArgPheSerArgHisSerThrIleuAspTyrIleAsnVal 415
 Db 1869 ACAGAAACCCCGAGGCCAGGCTCTCCCGGACAGCAGATCCGTGATTCATCATCAAGTGTG 1928
 QY 416 ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro 435
 Db 1929 GTCCCGACGGCTGGCCCCCTGGCTCAGAGGAGATGAGAAAGCCACACCAACAGCTCT 1968
 QY 436 ArgThrProLeuProProGlyAlaProSerProGluSerLysAsnGlnLysGln 455
 Db 1989 CGGACCCCTCTTCCACACAGGTCCTCCCTCCAGAAATCAAGAAAGAACCAAAAAACAG 2048
 QY 456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGln 475
 Db 2049 TATCAGTGGCCAGTTTCCAGAACCCAAATCATCTCCAAAGCCCAAGATCCACAGAG 2108
 QY 476 SerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu 495
 Db 2109 AGCCAAAGAGAGCTCCATGATGACACGCTCACTCCAGGCGTCAGAACCCAGGCGTAG 2168
 QY 496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512
 Db 2169 GCCCGGATGCCCAAGGGCCACCCAGCGGATTCACAGACAGCAAGTTCCAA 2219

RESULT 3

US-09-984-130-148

Sequence 148, Application US/09984130

Publication No. US20030055231A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OR INVENTION: 12 Human Secreted Proteins

FILE REFERENCE: PF489P2

CURRENT APPLICATION NUMBER: US/09/984,130

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 60/243,792

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: 09/836,353

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/198,407

PRIOR FILING DATE: 2000-04-19

PRIOR APPLICATION NUMBER: PCT/US99/25031

PRIOR FILING DATE: 1999-10-27

PRIOR APPLICATION NUMBER: 60/105,971

PRIOR FILING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 149

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 148

LENGTH: 2338

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

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LOCATION: (3)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

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LOCATION: (11)

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LOCATION: (12)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (17)

1024e)

OTHER INFORMATION: n equals a,t,g, or c
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 LOCATION: (38)
 OTHER INFORMATION: n equals a,t,g, or c
 US-09-984-130-148
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 Score: 2576.50 Matches: 509
 Percent Similarity: 73.17% Conservative: 1
 Best Local Similarity: 73.03% Mismatches: 2
 Query Match: 95.21% Indels: 185
 Gaps: 2
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 QY 21 PheTyrPleArgValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro 40
 Db 261 TTCTGATACGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 320
 QY 41 CysSerPheSerTyrProArgGlnAspTyrThrGlySerThrProAlaTyrGlyTyrTrp 60
 Db 321 TGCTCTTTCTCCACCCCGAAGAACTGACAGAGGCTACCCAGCTTATGCTACTG 380
 QY 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
 Db 381 TTCAAAGCAGTACTGAGACCAACCAAGGGGTCTCTGTGGCCCAACCAACCAAGAGTGA 440

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OY	101	CYSERLEUVALIIETARGSPALAGIINMETIINSPGIUSERGINTYRPHEPARGVAL	120
DB	501	TGCCTCTTGGTGATCAGAGACGCCAGATGCAGGATGATGATCAGTACTCTTTCGGGTG	560
OY	121	GLUARGGLYSERYVALARGTYRASNPHENECASNAPGLYPHEPHELEULYSVALTHR	140
DB	561	GAGGAGAGAACCTGTGTGAGATATATATTTCTGTGAACGATGGGTCTTCTTAAAGTAAACA	620
OY	141	ALALEUTHRGINLYSPROASPVALTYRILEPROGINTHRIENGLINPROGLYNPROVAL	160
DB	621	GCCTGACTCAGAAACCTCGATGTCTACTTCCCGAGACCTCGAGACCCGGGACCGGGTG	680
OY	161	THRVALILECYVALPHEASINTPALAPHEGLINLUCYSPROPIROSETPHESETRTP	180
DB	681	ACGGTCATCTGTGTGTTAACTGGGGCTTGAGAAATGTCCACCCCTTCTTCTCCG	740
OY	181	THRGLYVALALALEUSERSERGLCYLTHRYSPROTHRRPSTRHISPHESERVALLEU	200
DB	741	ACGGGGCTGGCTCTCTCTCCCAAGAAACCAACCAAGACTCTCCACTTTCAGTGTCC	800
OY	201	SERPHERTHRPROARGPROGIIINAPBHISAPHSRPHASPLEUTHRCYSHISVALASPHESER	220
DB	801	AGCTTCACGGCCCAACCCACGAGACACACAACCGACCTCACCTGCATGTGAGCTTCC	860
OY	221	ARGYSPGLYVALSERIALAGINARGTHRVALARGLEUARGVALALATYRALARPROARGSP	240
DB	861	AGAAAGGTTGAGACGTPACAGAGGACCGTCCGACTCGTGTGGCTATGCCCCAGANAC	920
OY	241	LEUVALIIESERIIIESERARGSPASINTHRPROASP	252
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OY	252		252
DB	1161	TACACCTGGCCGAGGGAGAACAGGCTTGGCTCCACGACGAGCCCTGGACCTCTCTGTG	1220
OY	253	-----PROPROGLIUAENLEUARGVALMETVALSERGINALIASARGTHRVALLEUGI	270
DB	1221	CAGTATCTCTCAGAGAACCTGAGAGTGATGTGTTTCCCAAGCAACAGSACAGTCTCTGAA	1280
OY	271	ASNLEUGIYASNGLYTHRSELEUPROVALLEUGIUGLYGINSEULEUCYSLEUVALCY	290
DB	1281	AACCTTGGGAAGGCGACGCTCTCTCCAGTACTGGAGGGCCAAACCTGTGCTGTCTGT	1340
OY	291	VALTHRIHISSESRPROPROALAIARGLEUSERTRPHRGINARGGLYGINVALLEUSER	310
DB	1341	GTCACACACAGACAGCCGCCACGAGCTGAGCTGGACCCAGAGGGGACAGAGTTCTGAGC	1400
OY	311	PROSERGINPROSEASPPROGLYVALLEUGIULEUPROARGVALGINVALGINISGLIN	330
DB	1401	CCCTCCACGACCTCAGAACCCCGGGAGTCTCGAGCTCGCTGGTTCAAGTGAACAGACGAA	1460
OY	331	GLYGLUPHERTHRCHYSHISALAIARGHISPROLEUGIYSERGINHISVALSERLEUSERLEU	350
DB	1461	GGAAAGTTCACTGCACAGCTCGGACCCACTGTGGGCTCCACAGCAAGTCTCTCAGCTCC	1520

Qy	351	SerAlaHisTyr	-----	354
Db	1521	TCCTGTGACATACCTCCCGAAGCTCTGGCCCTCTCTCTGGAGGCTGAGGCTCTG	-----	1580
Qy	354	-----	-----	354
Db	1581	CACATCGACACTCTCTCTCCCAAGCCAGCCGCCCTCTCTGCGCTGTGGCTTGGGGAG	-----	1640
Qy	354	-----	-----	354
Db	1641	GAGCTGCTGGAGGGGAACAGCAGCAGGACTCTTGAAGTCAACCCCAAGCTCAGCCGGG	-----	1700
Qy	354	-----	-----	354
Db	1701	CCCTGGGCAACAGCTCTCCCTGAGCCTCATGAGAGGCTCAAGCTCTGGCTCAAGCTCCGC	-----Lys 355	1760
Qy	355	-----	-----	355
Db	1761	TGTAGGCTGTGGAACTCCATAGGGGGCCAGAGTGGATCCATCTTCGACACTGCCAGATAAG	-----Lys 355	1820
Qy	356	LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla	-----	375
Db	1821	AAGGAGCTCATCTCAAGGCACTCTCCCAACGAGACGCTTCTGGAAATCGGATCAGCGCT	-----	1880
Qy	376	LeuLeuPheLeuCysIleAlaIleIleIleMetLysIleLeuProLysArgArgThrGln	-----	395
Db	1881	CTTCTTTTCTCTCTCTGGCCCTCATCATCATGTAAGATTTCTACCGAAGAGACGAGCTCAG	-----	1940
Qy	396	ThrGlnThrProArgProArgPheSerArgHisSerThrIleLeuAsnPyrIleAsnVal	-----	415
Db	1941	ACAGAAACCCCGAAGGCCAGGTTCTCCCGCAGACAGCATCTCGATTCATCATATGTG	-----	2000
Qy	416	ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro	-----	435
Db	2001	GTCCCGACGGCTGGCCCCCTGTGCTCAGAAAGGGAATCAGAAAGCCACACCAACAGTCT	-----	2060
Qy	436	ArgThrProLeuProProGlyAlaProSerProLysSerLysAsnGlnLysGln	-----	455
Db	2061	CGGACCCCTCTTCCACAGGCTCTCTCTCCCAATCAAGAAAGAACACGAAAAACAG	-----	2120
Qy	456	TyrGlnLeuProSerPheProGlnProLysSerSerThrGlnAlaProGlnSerGlnGlu	-----	475
Db	2121	TATACATGCCCAATTTCCCGAAGCCCAATCATCTCAAGCCCAAGATCCAGAGG	-----	2180
Qy	476	SerGlnGlnLeuLeuHisTyrAlaThrLeuAsnPheProGlyAlaArgProArgProGln	-----	495
Db	2181	AGCCAAAGAGAGCTCATTTATGCCACAGCTCAACTTCACAGGCGTCAGACCCAGGCTGAG	-----	2240
Qy	496	AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	-----	512
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; Sequence 1, Application US/09910600				
; Publication No. US2003003631A1				
; GENERAL INFORMATION:				
; APPLICANT: Longphre, Malinda				
; APPLICANT: Chang, Han				
; APPLICANT: Whitney, Gena				
; TITLE OF INVENTION: NOVEL STGLECS AND USES THEREOF				
; FILE REFERENCE: D0003ND				
; CURRENT APPLICATION NUMBER: US/09/910,600				
; CURRENT FILING DATE: 2001-07-20				
; PRIOR APPLICATION NUMBER: 60/220,139				
; PRIOR FILING DATE: 2000-07-21				
; NUMBER OF SEQ ID NOS: 32				
; SOFTWARE: PatentIn ver. 2.0				
; SEQ ID NO 1				
; LENGTH: 2565				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-09-910-600-1				

Alignment Scores:

Pred. No.: 4,24e-222 Length: 2565
 Score: 2278.00 Matches: 452
 Percent Similarity: 75.25% Conservative: 1
 Best Local Similarity: 75.08% Mismatches: 1
 Query Match: 84.18% Indels: 148
 DB: 11 Gaps: 2

US-09-937-636-3 (1-512) x US-09-910-600-1 (1-2565)

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 Db ATGCTACTGCGCAGCTGCTGCTCTGCTGCTGCGGGGCTCCAGGCTATGATGGAGGA 188
 QY 21 PheTrpIleArgValGlnGlnSerValMetValProGlnGlyLeuGlyIleSerValPro 40
 Db TTTCTGGATACGAGTGGAGGAGTCAGTGCTGGCGGAGGCTGTGATCTCTGTGCCC 248
 QY 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60
 Db TGCCTCTTCT 308
 QY 61 PheGlyAlaValTrpGlnTrpThrTrpGlyAlaProValAlaThrAsnHisGlnSerArg 80
 Db TTCAAGCAGCTGAGTGAACCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 368
 QY 81 GlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaValGlyAsn 100
 Db GAGGTGGAATGACACCGCCGCGGAGTCCAGCTCTGCGGATCCCGCCAGGGGAGAC 428
 QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
 Db TGCCTCTGCGGATCAGAGACGCGCAGATGAGATAGTACAGTACTCTCTCTCTCTCT 488
 QY 121 GlnArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuValThr 140
 Db GAGGAGGAGAGCTATGTGATATATATTCATGACACATGGTCTCTCTCTCTCTCT 548
 QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnTrpLeuGlnProGlyGlnProVal 160
 Db 548 ----- 548
 QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGlnCysProProPheSerPheSerTrp 180
 Db 548 ----- 548
 QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
 Db 549 -----GTGCTC 554
 QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
 Db 555 AGCTTACGCCCAACCCCGACGACACACACACCACTCACTCACTGATGGATTTCTCC 614
 QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
 Db 615 AGAAAGGGTGTGACCGACAGAGAGACCGTCCGACTCCGTGGCTATGCCCAAGAGAC 674
 QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp ----- 252
 Db 675 CTGTGTATACAGCATTTTCACTGACACACGCCACCCCTCGAGCCCAAGCCAGGAAAT 734
 QY 252 ----- 252
 Db 735 GTCCCATACTGGAAGCCCAAAAGGCCAAGTTCTCTGGGCTCTCTGTGCTGACAGC 794
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Db 855 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGGATTGAGGGCC 914
 QY 252 ----- 252
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 QY 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
 Db 975 CAGTATCTCCAGAGAACCTGAGAGTGTGTTTCCAGAGAACAGACAGCTCTGGAA 1034
 QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuCysLeuValCys 290
 Db 1035 AACCTGGGAACGACAGCTCTCTCCAGTACTGGAGGCGCAAACTGTGCTGCTGTGT 1094
 QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
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RESULT 5

US-09-978-295A-258

Sequence 258, Application us/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrata, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Mel-Olang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.93e-221	Length:	2764
Score:	2265.00	Matches:	450
Percent Similarity:	74.92%	Conservative:	1
Best Local Similarity:	74.75%	Mismatches:	3
Query Match:	83.70%	Indels:	148
	10	Gaps:	2

US-09-937-636-3 (1-512) x US-09-978-295A-258 (1-2764)

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Db 46 ATGCTACTGCGCAGTGGTGTCTGCTGCGTGGGGGCGGTCCAGCGCTATGATGGAGAGA 105
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Db 106 TTCTGTGATCAGTGCAGAGTATGATGTCGCCGAGGCGCTGTCCATCTCTGTCGCC 165
QY 41 CysSerPheSerIleProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60
Db 166 TGTCTTTCTCTCCACCCCAACAAGACTGGACAGGGGTCTACCCAGCTTATGGCTACTGG 225
QY 61 PheIleAlaValThrGlnTrpThrIleGlyAlaProValAlaThrAsnHisGlnSerArg 80
Db 226 TTCAAAGCACTGACTGACACCAAGGCGTCTCTGTGGCCCAAAACCAACGAGAGTCGA 285
QY 81 GluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaIleGlyAsn 100

Db 286 GAGGTGAATGACACCCGGCGCGATTCACAGTCACTGGGATCCCGCCAGGGGAGAC 345
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
Db 346 TGTCTCTGTGTATCAGAGACGGCGCAAGATCAGATGATGATCAGATCTCTTCCGGGTG 405
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Db 406 GAGAGAGGAAGCTATGTGACATTAATTTATGACAGTGGGTCTTTCTTAAGATACAA 465
QY 141 AlaLeuThrGlnIleProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
Db 465 ----- 465
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QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
Db 466 -----GTCCTC 471
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
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QY 221 ArgIleGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
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QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp ----- 252
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QY 252 ----- 252
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QY 252 ----- 252
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Db 772 TGGGGCCCTAGACCCCTGGGGCTGAGCTGCCGGGGTGAAGCTGGGATTCAGGGCGC 831
QY 252 ----- 252
Db 832 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCACAGCAGAGCCTTGACCTCTGTGG 891
QY 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
Db 892 CAGTATCTCCAGAAACCTGAGAGTATGTTTCCCAACAAACAGAGTATCTGGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyIleSerLeuCysLeuValCys 290
Db 952 AACCTTGGGAACGGCAGCTCTCTCCAGTCTGAGAGGCCAAAGCCCTGCTCTGT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
Db 1012 GTCAACACAGCAGCCCCCAGCCAGGCTGAGCTGAGCCCAAGAGGAGAGGTTCTGAGC 1071
QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnHisGln 330
Db 1072 CCTCCAGGCCCTCAGAGCCCGGGGCTCTGAGAGTGGCTGGGTGCAAGTGGAGACAGAA 1131
QY 331 GlyLeuPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
Db 1132 GGAAGATTCACTGCGCACCGCTCGCACCCACTGGGCTCCCAAGACGCTCTCTCAGGCTC 1191
QY 351 SerValHisTrpTrpLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370


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Db      1192 TCCGTCACATATAGAGAGGACTCATCTCACGCAATTCCTCCAGGAGCGTTCTGGGA 1251
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Db      1492 AACGAGAAACAGCATATGATGCTCCCATTTCCCGAAACCAATCATCCACTCAAGCC 1551
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Db      1552 CCAGAAATCCAGAGAGAGCCAGAGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTC 1611
QY      491 ArgProArgProGluAlaIleArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
Db      1612 AACACCGAGCGCTGAGGCCGCGGATGCCCAAGGACCCAGCGGATTATCAGAAAGTCAG 1671
QY      511 PheGln 512
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RESULT 6
US-09-978-697-258
Sequence 258, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: ROY, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
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; PRIOR APPLICATION NUMBER: 09/918585
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US-09-937-636-3 (1-512) x US-09-978-192A-258 (1-2764)

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RESULT 8

US-09-999-832A-258

; Sequence 258, Application US/0999832A

; Publication No. US20020192706A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697

Alignment Scores:

Pred. No.:	9,936-221
Score:	2265.00
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Best Local Similarity:	78.75%
Query Match:	83.70%
DB:	10
	Gaps: 2
	Length: 2766
	Matches: 450
	Conservative: 1
	Mismatches: 3
	Indels: 148
	Gaps: 2

US-09-937-636-3 (1-512) x US-09-999-832A-258 (1-2764)

Qy	1	MetLeuLeuProLeuLeuLeuSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	20
Db	46	ATCTACTCCCACTGCTGCTCTCCGCTGCGGGCGGGTCCACAGCATGATGAGGGAGA	105
Qy	21	PheTrpIleArgValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro	40
Db	106	TTCGTGATACGAGTCAGAGTCAGTGGTGGCGGAGGGCTGTGCATTTCTGTCCC	165
Qy	41	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTCTCTACCCCGACACAGACTGAGAGGGTCTACCCAGCTTATGGCTACTGG	225
Qy	61	PheValAlaValThrGluThrThrItySglYalaProValAlaAlaThrAsnHisGlnSerArg	80
Db	226	TTTCAAAAGCAGTGCATGACGACCAACGAGGGTGTCTCTGGCCACAAACACACACAGTCTGA	285
Qy	81	GluValGlnMetSerThrArgIlyArgIlyrPheGlnLeuThrGlyAspProAlaGlyAsn	100
Db	286	GAGGTGGAATGAGCCACCCGGGGCGGATTCACGCTCACTGGGGATCCCGGCACAGGGGAAAC	345
Qy	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal	120
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Qy	121	GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuValThr	140
Db	406	GAGAGGAGAGCATATTCATATTAATTTCAATGAACAGATGGCTTCTTTTAAAAGTAAACA	465

QY	141	AlaLeuThrGlnLysProAspValLyrTrIleProGluThrLeuGluProGluInProVal	160
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QY	161	ThrValIleCysValAlpheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp	180
Db	465	-----	465
QY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrTrhSerHisPheSerValLeu	200
Db	466	-----GTGCTC	471
QY	201	SerPheThrProArgProGlnAspHisAspTrhAspLeuThrCysHisValAspPheSer	220
Db	472	AGCTTACAGCCCGACGCCAGACACACACACACGACCTCACCTGGCAATGTGGACTCTCC	531
QY	221	ArgLysGlyValSerAlaGlnArgTrhValArgLeuAlaGValAlaLysTrpAlaProArgAsp	240
Db	532	AGAAAGGTTGTGAGGGCACAGAGACCGTCCGACTCCGTGTGGCTATATGCCCCAGAGAC	591
QY	241	LeuValIleSerIleSerArgAspAsnTrhProAsp	252
Db	592	CTGTATTACACATTTCACGTGCACAAACAGCCAGCCCTGGAGCCCCAGCCCAAGGAAT	651
QY	252	-----	252
Db	652	GTCCCATACGTGAAGCCCAAAAGGCCAGTTCTGTGGGCTCTGTGTGCTGTACAGC	711
QY	252	-----	252
Db	712	CAGCCCCCTGCCACACTAGCTGGGTCTGCAGAAACAGAGTCTCTCTCGTCCATCCC	771
QY	252	-----	252
Db	772	TGGGGCCCTAGACCCCTGGGGCTGTAGAGTCCCGGGGTGAAGAGCTGGGGATTCAAGGGCC	831
QY	252	-----	252
Db	832	TACACCTGCGGAGGAGACAGAGCTTGCTCCAGACAGAGCCCTGGACTCTCTGTG	891
QY	253	-----ProproGluAsnLeuArgValIleValSerGlnAlaAsnArgTrhValLeuGlu	270
Db	892	CAGTATCTCCAGAAACCTGAGACTGATGGTTCCCAAGCAACAGACAGCACTCTCGAA	951
QY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlnGlnSerLeuCysLeuValCys	290
Db	952	AACCTGGGAAGGAGCACTCTCTCCAGTACTGAGAGGGCAAAAGCCTGGCTGTGCTGT	1011
QY	291	ValTrhHisSerSerProProAlaArgLeuSerTrpTrhGlnAlaGlyGlnValLeuSer	310
Db	1012	GTCAACACACAGACCCCGCCAGCCAGGCTGAGCTGAGACCCAGAGGGGACAGGTTCTGAGC	1072
QY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnGlnGlu	330
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QY	331	GlyGluPheTrhCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1132	GGAGAGTTCACTGCCAGCTGTGGACCAACCACCTGGGGCTCCAGACAGTCTCTCAAGCTC	1193
QY	351	SerValHisTrpLysLysGlyLeuIleSerTrhAlaPheSerAsnGlyValAlaPheLeuGly	370
Db	1192	TCCGTGCACTTAAAGAGGACTATCTCAAGGCAATCTCCAAAGGAGAGCTTCTGGGA	1253
QY	371	IleGlyIleTrhAlaLeuLeuPheLeuCysLeuAlaLeuIleIleLeuLysIleLeuPro	390
Db	1252	ATCGGCATCAGGGCTCTTCTTCTCTGCTGCGCCCTGATCATATGAAAGATTCTACCG	1313
QY	391	LysArgAspTrhGlnThrGluThrProArgProAspPheSerArgHisSerTrhIleLeu	410
Db	1312	AAGAGACGCACTCAACAGAAACCCCGAGGCCAGGTTTCTCCGGCACAGCAAGTCTCTG	1373
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QY 491 ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510
Db 1612 AGACCCAGGCTGTAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAAGAGTCAAG 1671
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; Sequence 258, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavyn, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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OY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
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OY 252 ----- 252
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OY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGluGlnSerLeuGluValCys 290
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OY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyValIleLeuSer 310
DB 1012 GTCAACACACAGAGCGCCCGACCGGCTGAGCTGAGCCACAGAGGGACAGTTTCTGAGC 1071
OY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHisGlu 330
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OY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
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OY 371 IleGlyIleThrAlaLeuLeuPheLeuGluLeuAlaLeuIleIleMetLysIleLeuPro 390
DB 1252 ATCGGCATACAGGCGCTCTCTCTCTCTGCTGCGCCCTGATCATCATGAAGATTCACCG 1311

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OY 411 AspTyrIleAsnValAlaProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
DB 1372 GATTACATCATATGTGTCTCCGAGCGGTGGCCCTCTGCTCAGAGGGAATCAGAAAGCC 1431
OY 431 ThrProAsnSerProArgThrThrProLeuProProGlyValAlaProSerProGluSerLys 450
DB 1432 ACACCAAAAGTCTCGAGACCCCTCTCCACAGGAGTCTCCCTCCAGAAATCAAGAG 1491
OY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
DB 1492 AACCAAGAAACACAGTATCAGTTGCCAGTTTCCAGAAACCAAAATCATCTCAAGCC 1551
OY 471 ProGluSerGlnLysSerGlnGluLeuLeuHisTyrAlaThrLeuAsnPheProGlyVal 490
DB 1552 CCAGAAATCCAGAGAGAGCCCAAGAGAGCTCATTTATGCCAGCTCAACTTCCAGGCTC 1611
OY 491 ArgProArgProGluValAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510
DB 1612 AGACCCAGGCGCTGAGGCGCCGATGCCCAAGGGGACCCAGGCGGATATGCAAGATCAAG 1671
OY 511 PheGln 512
DB 1672 TTTCAA 1677

RESULT 11
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: Sequence 258, Application US/09978585A
: Publication No. US20030049633A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gottlieb, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C15
: CURRENT APPLICATION NUMBER: US/09/978,585A
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 258
: LENGTH: 2764
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-978-585A-258

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APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavik, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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44 PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores:	
Pred. No.:	9,93e-221
Score:	2285.00
Percent Similarity:	74.928
Best Local Similarity:	74.754
Query Match:	83.704
DB:	11
	Gaps:
	2

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Db	46	ATCTCTACTCCACTGCTGCTGTCTCCCTGCTGGGGGGGTCCAGGCTATGAGAGGAGA	105
QY	21	PheTrpAlaArgValGlnGlnSerAlaMetAlaProGlnGlyLeuAlaCysIleSerValPro	40
Db	106	TTCGTGATTCAGATGACGAGAGCATGTGATGGTGGCGGAGGCGCTGTGCATCTGTGCCC	165
QY	41	CysSerPheSerTyrProArgGlnAspIrrpIrrpIrrpGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTTTCTCTACCCCGGACAAACCTGGACAGGGGTTCACCCAGCTTATGGCTACTGG	225
QY	61	PheGlyAlaValAlaThrGluThrIleGlySerGlyAlaProValAlaIrrpAsnHisGlnSerArg	80
Db	226	TTCAAAAGCATGACTGAGCAACAAGAGGTGCTCCTGTGGCCACAAACCCACAGAGTCGA	285
QY	81	GluValGlnMetSerThrArgGlyIrrpPheGlnLeuThrGlyAspProAlaIrrpGlyAsn	100

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QY	121	GluArgGlySerTyrValArgTyrAspPheMetAspAspGlyPhePheLeuValILhr	140
Db	406	GAGAGAGAAAGCTATGTGACATTAATTAATTATGAAACAGAGGGTTCTTTCTTAAAGTAACA	465
QY	141	AlaLeuThrGlnLysProAspValTyrILleProGluThrLeuGluProGlyInProVal	160
Db	465	-----	465
QY	161	ThrValILleCysValPheAsnTTPAlaPheGluGluCysProProSerPheSerTTP	180
Db	465	-----	465
QY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValILeu	200
Db	466	-----GTGCTC	471
QY	201	SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220
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QY	252	-----	252
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Db	832	TACACCTGCCGAGCGAGAAAGAGCTTGGCTCCAGACAGACGACCTTGACTCTCTGTG	891
QY	253	-----ProProGluAsnLeuArgValILMetValSerGlnAlaAsnArgThrValLeuGlu	270
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OY 371 IleglylethralaleuPheucysleuAlaleuIlellewetylleuPro 390
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RESULT 13
US-09-978-403A-258
Sequence 258, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

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QY 252 ----- 252
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Db 1672 TTCCAA 1677
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; Sequence 258, Application US/09978564A
; Publication No. US20030050241A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Alignment Scores:

Pred. No.: 9.93e-221 Length: 2764
Score: 2265.00 Matches: 450
Percent Similarity: 74.92% Conservative: 1
Best Local Similarity: 74.75% Mismatches: 3
Query Match: 83.70% Indels: 148
DB: 11 Gaps: 2

US-09-937-636-3 (1-512) x US-09-978-564A-258 (1-2764)

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Db	46	ATGCTACTGCCACCTCTGCTGTCTCTGCTGCTGGCGGGTCTCCAGGCTTGGATGGGAGA	105
Oy	21	PheThrIleArgValGlnGluSerValMetValProGluGlyLeuysIleSerValPro	40
Db	106	TTCTGGAATACGAGTGCAGAGTCACTGATGATGCGGAGAGGGCTGTGATCTCTGTGCCC	165
Oy	41	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTCTCTCTACCCCCCGACAACTGGACAGGGTCTACCCCACTTATGGCTACTGG	225
Oy	61	PheIysAlaValThrGluThrThrIleArgGlyAlaProValAlaThrAsnHisGlnSerArg	80
Db	226	TTCAAAGCAGTCACTGAGACAACCAAGGGTGTCTCTGTGGCCACAACCAACCAAGATCGA	285
Oy	81	GluValGluMetSerThrArgGlyLysArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	100
Db	286	GAGGTGGAAATAGACACACCGGGGGCGGATTCACAGCTCAGCTGGGGATCCCGCAAGGGGAA	345
Oy	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	120
Db	346	TGCTCTCTTGGTATCAGAGACGCGCAGATGAGATGAGTACAGATCACTTCTTCCGGTTC	405
Oy	121	GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr	140
Db	406	GAGAGAGAAAGCTATGTGACATATTAATTCATGCAAGAGATGGGTCTCTTCTTAAAGTAACA	465
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Oy	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	200
Db	466	-----GTCCTC 471	471
Oy	201	SerPheThrProArgProGlnAspHisAspTrpAspLeuThrCysHisValAspPheSer	220
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Db	532	AGAAAGGTGTAGCGCACAGAGAGACCGTCCGACCTCCGTGGCTATGCCCCACAGAC	591
Oy	241	LeuValIleSerIleSerArgAspAsnThrProAsp-----	252
Db	592	CTTGTTATCAGCATTTCACTGACACAACACGACCGCTGAGAGCCCAAGCCCAAGGAAAT	651
Oy	252	-----	252
Db	652	GTCCTATACCTGGAAAGCCAAAAGGCCAGTTTCTGCGGCTCTCTGTGCTGTGACAGC	711
Oy	252	-----	252
Db	712	CAGCCCCCGCACACTGAGTGGGTCCGCGAAGACAGAGTCTCTCTGCTGCTCCATCCC	771
Oy	252	-----	252
Db	772	TGGGCGCTAGACCCCTGGGCGCTGGAGCTGCCCCGGGTGAAGCTGGGATTCAGGGCGC	831
Oy	252	-----	252
Db	832	TACACCTGCCGAGCGGAGAACAGGCTTGCTGCCACAGCCAGGACCTTGACCTCTGTG	891
Oy	253	-----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	951
Db	892	CAGTATCTCCCAAGACAACTGAGATGATGATTTCCCAAGCAACAGACAGTCTGGAA	951
Oy	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuGlyLeuValCys	290
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Db	952	AACCTTGGGAACGGACACTCTCTCCCACTACTGGAGGGCCAAAGCCTGTGCTGTCTGT	101
Qy	291	ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	310
Db	1012	GTCACACACAGACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGAGAGGTTCTTGAGC	1071
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Qy	351	SerValHisTrpTrpLysGlyLeuLeuLeuSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
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Qy	391	LysArgArgGlyThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu	410
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Qy	491	ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTrpAlaGluValLys	510
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; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Baker Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleon			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Maty E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Kuo, Sophia S.			

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
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QY      511 PheGln 512
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Search completed: October 8, 2003, 22:50:19
 Job time : 477 secs